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(54) Methods of testing for bronchial asthma or chronic obstructive pulmonary disease

(57) An objective of the present invention is to provide a method of testing for bronchial asthma or chronic obstructive pulmonary disease, a method of screening for candidate compounds for treating bronchial asthma or chronic obstructive pulmonary disease, and a pharmaceutical agent for treating bronchial asthma or chronic obstructive pulmonary disease.

The present invention identified genes whose expression levels varied between respiratory epithelial cells that had been stimulated by IL-13 to induce the goblet cell differentiation, and unstimulated respiratory epithelial cells. The respiratory epithelial cells were cultured according to the air interface method. The genes were revealed to be useful as markers for testing for bronchial asthma or chronic obstructive pulmonary disease and screening for therapeutic agents for such diseases. Specifically, the present invention provides methods of testing for bronchial asthma or chronic obstructive pulmonary disease and methods of screening for compounds to treat the diseases based on the comparison of the expression levels of marker genes identified as described above. .

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Description

FIELD OF THE INVENTION

[0001] The present invention relates to methods of testing for bronchial asthma or chronic obstructive pulmonary disease (COPD).

BACKGROUND OF THE INVENTION

[0002] Currently, there are more than one hundred million bronchial asthma patients in the world. The rapid increase in the number of asthma patients is a social problem in Japan as well. In advanced countries, the number has increased by 20-50% in the past decade. Thus, asthma is thought to be one of the diseases that would pose a major health threat in the 21st century.

[0003] Pharmaceuticals used today for treating asthma and candidate pharmaceuticals for that purpose, include: inhaled steroids and oral steroids; agents that suppress the release of inflammatory mediators; anti-allergy agents such as histamine H1 antagonists; β2 agonists that act as bronchodilators; and immunosuppressive agents. According to a report describing clinical cases in New Zealand, the widespread use of inhaled steroids and β2 agonists has decreased the mortality rate of patients by 30% compared to 10 years ago. However, both inhaled steroids and β2 agonists have been reported to have side effects. The side effects of inhaled steroids include oral and esophageal candidiasis, olfactory disorders, adrenal suppression, osteoporosis, cataract, glaucoma, skin thinning, and growth inhibition in children. Side effects of β2 agonists include ischemic diseases, hyperthyroidism, and diabetes mellitus. In addition, regular use of β2 agonists has been known to reduce the efficacy of these drugs.

[0004] Bronchial asthma is characterized by respiratory inflammation and airflow obstruction resulting from various degrees of respiratory stenosis. Representative symptoms include paroxysmal cough and difficulty in breathing. The degree of airflow obstruction in bronchial asthma ranges from relatively mild to life-threatening obstructions. Furthermore, it has been reported that allergic reactions in the mucous membrane of the respiratory tract and bronchial smooth muscles are closely involved in bronchial asthma development.

[0005] Specifically, an atopic disposition accompanied by hyperproduction of IgE antibodies is seen in many bronchial asthma patients. Many causes are thought to lead to bronchial asthma, but there is no doubt that an atopic disposition is one cause of hypersensitivity in many patients. It is predicted that contraction of bronchial smooth muscles, edema of the respiratory tract mucous membrane, or respiratory tract hypersecretion is involved in the mechanism of respiratory obstruction in an asthma attack. Type-I allergic reactions in the respiratory tract due to exposure to pathogenic allergens play an important role in such changes in the respiratory tract.

[0006] In bronchial asthma patients, the activity of Th2 helper T cells is enhanced, and so is the production of Th2 cytokines such as interleukin-3 (hereinafter abbreviated as "IL-3"; similarly, interleukin is abbreviated as "IL") , IL-4, IL-5 , IL-13 and granulocyte macrophage colony stimulating factor (GM-CSF), and chemokines such as eotaxin and RANTES. IL-4 and IL-13 have the activity of inducing IgE production, and IL-3 and IL-4 have the activity of inducing the proliferation of mast cells. Eosinophils that differentiate and proliferate by IL-5 and GM-CSF infiltrate into the respiratory tract by the action of eotaxin and RANTES (Allergy Asthma. Proc. 20: 141 (1999)).

[0007] Eosinophils that infiltrate into the respiratory tract release intracellular granule proteins such as activated major basic protein (MBP) and eosinophil cationic protein (ECP) as a result of degranulation (Compr. Ther. 20: 651 (1994)). These granule proteins exhibit cytotoxic activity, and thus, ablate and damage epithelial cells. The ablation of epithelial cells results in the exposure of sensory nerve endings, enhances the permeability of the epithelium, and causes the loss of the epithelium-derived smooth muscle relaxing factor. Furthermore, eosinophils are known to secrete leukotriene C4 (LTC4) and Platelet activation factor (PAF), which have the activity of enhancing bronchial smooth muscle constriction, and platelet activating factor (PAF). It has been suggested that these reactions are repeated in the body and become chronic resulting in bronchial wall thickening and respiratory hypersensitivity.

[0008] Specifically, several reports have suggested the deep involvement of IL-4 and IL-13 in allergic reactions. For example, it is known that respiratory hypersensitivity disappears in IL-4-knockout mice (Yssel, H. and Groux, H., Int. Arch. Allergy Immunol., 121: 10-18, 2000). In a mouse model, IL-13 has been shown to be involved in forming an asthma-like pathology regardless of IgE production and the Th2 type (Wills-Karp, M. et al., Science, 2822: 2258-2261, 1998; Grunig, G. et al., Science, 282: 2261-2263, 1998; Zhu, Z. et al. , J. Clin. Invest., 103: 779-788, 1999). In addition, IL-4 receptors and IL-13 receptors are highly expressed in human respiratory epithelial cells and bronchial smooth muscles (Heinzmann, A. et al. , Hum. Mol. Genet., 9: 549-559, 2000). Accordingly, these tissues are thought to be the targets of IL-4 and IL-13. On the other hand, SNPs present in IL-4 receptor α and IL-13 have been shown to be one of the genetic causes of allergic diseases (Mitsuyasu, H. et al., Nature Genet., 19: 119-120, 1998; Mitsuyasu, H. et al., J. Immunol. , 162: 1227-1231, 1999; Kruse, S. et al . , Immnol., 96: 365-371, 1999; Heinzmann, A. et al., Hum. Mol. Genet., 9: 549-559, 2000).

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[0009] Furthermore, IL-4 and IL-13 have been reported to suppress the expression of the β and γ subunits of amiloride-sensitive epithelial sodium channel (ENaC) and increase the expression of cystic fibrosis transmembrane conductance regulator (CFTR) in tracheal epithelial cells. This suppresses Na^+ release and enhances Cl^- secretion. As a result, water secretion is assumed to increase in the bronchial lumen (Galietta L. J. V. et al., J. Immunol. 168: 839-45 (2002)). Therapeutic agents that target the signaling molecules of IL-4 or IL-13, such as IL-4 agonists, soluble IL-4 receptor α (Borish L. C. et al. , Am. J. Respir. Crit. Care Med. 160: 912-22 (1999)) , soluble IL-13 receptor α2, anti-IL-13 antibodies, and anti-IL-4 antibodies, have already been clinically applied and are expected to be effective in treating bronchial asthma.

[0010] Inflammation in the respiratory tract is known to elevate the expression levels of cytokines and adhesion molecules. Genes encoding such cytokines and adhesion molecules, which participate in the onset of allergic diseases such as bronchial asthma, can be targets in drug discovery. Specifically, patients can be diagnosed for the onset of symptoms, seriousness, response to medical treatments, or such, by detecting variations in the expression levels of these genes. Furthermore, patients can be treated using a substance that controls the expression level of such genes or regulates protein activity.

[0011] There are several commercially available expectorants for removing sputum, the cause of death by suffocation in asthma. However, until recently, available expectorant types were restricted to those that contain an active SH group, and those that hydrolyze or lubricate the mucus. However, "fudosteine" (a low-molecular-weight oral drug), which was jointly developed by two Japanese pharmaceutical companies, SS Pharmaceutical Co. Ltd.,and Mitsubishi Pharma Corporation, and released last December, is a pharmaceutical agent having an activity to suppress goblet cell hyperplasia.

[0012] In addition, Genaera Corporation in the United States has reported that the hCLCA1 gene is closely associated with the production of IL-9 and mucus in the mucosal epithelia in asthma patients (J. Allergy Clin. Immunol. 109: 246-50 (2002)) ; the hCLCA1 gene is the human counterpart of Gob-5 reported by Takeda Chemical Industries LTD. , Japan (Proc. Natl. Acad. Sci. USA 98: 5175-80 (2001)). Furthermore, clinical trials have already been launched for the low-molecular-weight oral drug "LOMUCIN" that inhibits the function of this gene.

[0013] In the bronchia of asthma patients, the aggravation of the disease state induces differentiation of respiratory epithelial cells into goblet cells and proliferation of these cells. Goblet cells produce a huge glycoprotein called mucin. This protein contributes to the production of sputum, which causes breathing difficulties and is a leading cause of death in chronic bronchial asthma. The increase in the number of goblet cells, which are secretory cells, enhances secretions in the respiratory tract. Thus, such secreted material enhances the obstruction of the respiratory tract and largely contributes to the worsening of asthma symptoms. However, the mechanism underlying goblet cell differentiation in the respiratory epithelium is still unknown.

[0014] The term "chronic obstructive pulmonary disease" refers to mainly pulmonary emphysema and chronic bronchitis. Shortness of breath is a main symptom of pulmonary emphysema; cough and sputum are main symptoms of chronic bronchitis. These are the major subjective symptoms of respiratory diseases in aged patients. In addition to aging, smoking is deeply involved in the onset of chronic obstructive pulmonary diseases. In pulmonary emphysema, the walls of pulmonary alveoli at the end of bronchioles are damaged and greatly swollen; the elasticity and contractility of the walls are impaired, and thus, the lungs have difficulty contracting during exhalation. This often causes shortness of breath. In addition, bronchial disorders result in bronchial obstruction, which is caused by swollen mucous membranes, sputum, and such. In chronic bronchitis, chronic inflammation and edema in the bronchia induce differentiation of bronchial epithelial cells into goblet cells, which results in the overproduction of secretory material. This results in coughs that produce sputum. In chronic obstructive pulmonary diseases, narrowed bronchia and damaged lungs cannot be restored to the original state. Furthermore, there are about 220,000 and 1,400,00 patients with chronic obstructive pulmonary diseases in Japan and the United States, respectively, and the diseases are the fourth leading cause of death in both countries. Thus, chronic obstructive pulmonary diseases are quite serious.

[0015] There is a report suggesting the correlation between chronic obstructive pulmonary diseases and IL-13 (Zheng T. et al, J Clin. Invest.; 106, 1081-1093, 2000). According to this report, transgenic mice in which respiratory epithelial cells were allowed to express IL-13, developed pulmonary emphysema, inflammation, and goblet cell hyperplasia.

SUMMARY OF THE INVENTION

[0016] As described above, in bronchial asthma or chronic obstructive pulmonary diseases, changes in respiratory epithelial cells are crucial factors constituting the disease states. One of the morbid changes of respiratory epithelial cells is the differentiation into goblet cells. An objective of the present invention is to identify genes associated with the differentiation into goblet cells. Another objective of the present invention is to provide diagnostic markers for bronchial asthma and drug discovery targets.

[0017] Drugs suppressing the differentiation into goblet cells in respiratory epithelial tissues were developed only recently. This is a new approach in drug discovery. Once the mechanism underlying the differentiation into goblet cells

is elucidated, it may be possible to establish a basic treatment for bronchial asthma. Furthermore, agents that affect the process of goblet cell differentiation are predicted to be useful in the treatment of diseases involving inflammation and overproduction of mucus, such as chronic obstructive pulmonary diseases, cystic fibrosis, chronic sinusitis, bronchiectasis, diffuse panbronchiolitis, as well as asthma.

[0018] A culture method (called the "air interface (AI) method") for differentiating human respiratory epithelial cells into goblet cells in the presence of IL-13 has been established by researchers of the Department of Geriatric and Respiratory Medicine, Tohoku University School of Medicine, Japan, who are collaborators in the present invention. Using this method, the present inventors predicted that goblet cell differentiation-associated genes can be identified by elucidating which gene expression varies in respiratory epithelial cells when stimulated by IL-13.

[0019] Conventionally, bronchial epithelial cells played a vital role in studies concerning the transport of water and electrolytes in humans and other animals. Moreover, particularly in humans, these cells have been significant in clarifying disease states of respiratory tract infections in cystic fibrosis and in establishing therapeutic methods. Over the past two decades, methods for culturing (*in vitro*) respiratory epithelial cells obtained from protease-treated trachea tissues have been improved by improving culture media and using growth-promoting substances. In addition, the AI method has been established, in which cilia and secretory granules can be produced *in vitro* by culturing cells under conditions similar to the environment around respiratory epithelial cells *in vivo*. In the AI method, the culture medium facing the mucous membrane side (apical side) of the cells is removed exposing cells to air while water and nutrients are supplied from the chorionic membrane side (basolateral side) (Van Scott MR., Exp Lung Res, 11: 75-94, 1986, Widdicombe JH., Am J Physiol, 258:L13-L18, 1990, Kim KC, J Biol Chem, 260: 4021-4027, 1985, Adler KB, Am J Respir Cell Mol Biol, 2:145-154, 1990).

[0020] Human bronchial epithelial cells cultured in the presence of human IL-13 using the air interface method were reported to express TGF-α (Booth BW, Adler KB, Bonner JC, Tournier F, Martin LD. Interleukin-13 induces proliferation of human airway epithelial cells in vitro via a mechanism mediated by transforming growth factor-α. Am J Respir Cell Mol Biol . 2001 Dec; 25(6): 739-743). In addition, the ion transport ability of human bronchial epithelial cells has been evaluated in a previous report, in which cells were cultured by the air interface method in the presence of IL-13 (Danahay H, Am J Physiol Lung Cell Mol Physiol, 282:L226-L236, 2002). However, these reports make no reference to goblet cell differentiation, and have not conducted any exhaustive gene expression analyses.

[0021] Furthermore, bronchial epithelial cells of guinea pigs has been reported to differentiate into goblet cells when cultured in the presence of human IL-13 for 14 days using the air-liquid interface method (Kondo, M., Tamaoki, J., Takeyama, K., Nakata, J. and Nagai, A. Interleukin-13 induces goblet cell differentiation in a primary cell culture from Guinea pig tracheal epithelium. Am J Respir Cell Mol Biol 27,536-541, 2002). However, there are no reports on exhaustive analyses of genes expressed in human bronchial epithelial cells cultured by the method described above.

[0022] On the other hand, the present applicants have identified eight types of allergy-associated genes whose expression levels decrease upon IL-4 or IL-13 stimulation in several lots of primary human respiratory epithelial cell cultures (Unexamined Published Japanese Patent Application No. (JP-A) 2002-191398). The applicants have also identified six types of allergy-associated genes whose expression levels greatly increase in several lots under the same conditions as described above (WO 02/052006 A1). The gene expression analyses in these two previous patent applications were carried out using a conventional culture method which induces no goblet cell differentiation.

[0023] Using oligonucleotide microarrays (GeneChip®, Affymetrix, Inc.) and air interface method, the present inventors compared the expression profiles of genes expressed in respiratory epithelial cells stimulated with IL-13 for goblet cell differentiation, with those of cells not stimulated with IL-13. The inventors selected genes whose expression levels increased by two folds or more or decreased by half or more of the initial levels as a result of the differentiation, and determined the expression levels of the genes. Then, the inventors confirmed the variation of the expression level of marker genes selected from the group described below in (a) or (b).

[0024] Furthermore, with respect to the mouse homologs of the human genes selected by the method described above, the inventors detected variations in the expression levels in respiratory hypersensitivity model mice. As a result, the variation pattern of expression levels of the mouse homologs coincided well with that of human genes.

[0025] The nucleotide sequences of the respective marker genes listed in (a) and (b) are known. The functions of the proteins encoded by each marker gene are described in the references listed in the "References" section in Tables 3-19 (increased) and Tables 20-36 (decreased) below. The nucleotide sequences of the mouse homologs of the marker genes of the present invention are also known. The functions of the proteins encoded by the mouse homologues of the respective marker genes are described in the references listed in the "References" section in Tables 40-62 (increased) and Tables 63-83 (decreased) below.

[0026] Among these groups of genes, some genes have been reported to be directly related to bronchial asthma. However, most of the genes have not been shown to be associated with an allergic disease. Furthermore, even for genes that are reported to be associated with bronchial asthma, there are no reports that focus on the aspect of combinations with other co-expressing genes whose expression levels vary at the same timing that the asthma-related genes do.

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[0027] A close relationship between bronchial asthma symptoms and the marker genes of the present invention is suggested by the finding that the expression levels of marker genes vary in the differentiation process of respiratory epithelial cells into goblet cells. The relationship between the allergic response of the respiratory epithelium and the marker genes of the present invention was verified by the fact that the variation pattern of the expression levels of mouse homologs in the respiratory hypersensitivity mouse model is consistent with that in humans. Based on the findings described above, the present inventors revealed that tests for bronchial asthma or chronic obstructive pulmonary disease and screenings for therapeutic agents can be achieved by using as a marker the expression level of each marker gene or the activity of the protein encoded by each marker gene.

[0028] Specifically, the present invention relates to the following methods of testing for bronchial asthma or chronic obstructive pulmonary disease and the following methods of screening for candidate compounds for treating bronchial asthma or chronic obstructive pulmonary disease:

[1] a method of testing for bronchial asthma or chronic obstructive pulmonary disease, which comprises the steps of:

(1) determining the expression level of a marker gene in a biological sample from a subject;
(2) comparing the expression level determined in step (1) with the expression level of the marker gene in a biological sample from a healthy subject; and
(3) judging the subject to have bronchial asthma or chronic obstructive pulmonary disease when the result of the comparison in step (2) indicates that (i) the expression level of the marker gene in the subject is higher than that in the control when the marker gene is a gene according to (a) or (ii) the expression level of the marker gene in the subject is lower than that in the control when said marker gene is a gene according to (b);

wherein the marker gene is any one selected from the group according to (a) or (b) :

(a) a group of genes whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13, and comprise any one of the nucleotide sequences of SEQ ID NOs: 25 to 310;
(b) a group of genes whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13 and comprise any one of the nucleotide sequences of SEQ ID NOs: 311 to 547;

[2] the testing method according to [1], wherein the biological sample is a respiratory epithelial cell;
[3] the testing method according to [1], wherein the gene expression level is measured by PCR analysis of the cDNA;
[4] the testing method according to [1], wherein the gene expression level is measured by detecting the protein encoded by the marker gene;
[5] a reagent for testing for bronchial asthma or chronic obstructive pulmonary disease, wherein the reagent comprises a polynucleotide comprising the nucleotide sequence of a marker gene, or an oligonucleotide having at least 15 nucleotides and comprising a nucleotide sequence complementary to the complementary strand of the nucleotide sequence of the marker gene, and wherein, the marker gene is any one selected from the group according to (a) or (b) in [1];
[6] a reagent for testing for bronchial asthma or chronic obstructive pulmonary disease, wherein the reagent comprises an antibody that recognizes a protein encoded by a marker gene, and wherein the marker gene is any one selected from the group according to (a) or (b) in [1];
[7] a method of screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, wherein the marker gene is any one selected from the group according to (a) or (b) in [1], and wherein the method comprises the steps of:

(1) contacting a candidate compound with a cell expressing the marker gene;
(2) measuring the expression level of said gene; and
(3) selecting a compound that decreases the expression level of a marker gene belonging to group (a) or increases the expression level of a marker gene belonging to group (b), as compared to that in a control with which the compound has not been contacted;

[8] the method according to [7], wherein the cell is a respiratory epithelial cell or a goblet cell;
[9] the method according to [8], which comprises the step of culturing the respiratory epithelial cells under conditions in which culture medium is removed from the apical side of said cells and the culture medium is supplied from the basolateral side of the cells;
[10] a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease, wherein the kit comprises (i) a polynucleotide comprising the nucleotide sequence

of a marker gene, or an oligonucleotide having at least 15 nucleotides and comprising a nucleotide sequence that is complementary to the complementary strand of the polynucleotide, and (ii) a cell expressing the marker gene, and wherein the marker gene is any one selected from the group according to (a) or (b) in [1];

[11] a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease, wherein the kit comprises (i) an antibody that recognizes a protein encoded by a marker gene, and (ii) a cell expressing the marker gene, wherein the marker gene is selected from the group according to (a) or (b) in [1];

[12] the kit according to [10] or [11], which further comprises a cell-supporting material to culture respiratory epithelial cells under conditions in which the culture medium is supplied from the basolateral side of the cells;

[13] the kit according to [12], which further comprises respiratory epithelial cells;

[14] an animal model for bronchial asthma or chronic obstructive pulmonary disease, wherein the animal is a transgenic nonhuman vertebrate wherein the expression level of a marker gene, or a gene functionally equivalent to the marker gene, has been increased in the respiratory tissue, wherein the marker gene is any one selected from the group according to (a) in [1] or the following (A):

(A) a group of genes whose expression levels increase in the lung of an animal model for bronchial hypersensitivity induced by an exposure to the ovalbumin antigen, wherein the genes comprise any one of the nucleotide sequences of SEQ ID NOs: 954 to 1174;

[15] the animal model according to [14], wherein the nonhuman vertebrate is a mouse;

[16] an animal model for bronchial asthma or chronic obstructive pulmonary disease, wherein the animal is a transgenic nonhuman vertebrate wherein the expression level of a marker gene, or a gene functionally equivalent to the marker gene, has been decreased in the respiratory tissue, wherein the marker gene is any one selected from the group according to (b) in [1] or the following (B):

(B) a group of genes whose expression levels decrease in the lung of an animal model for bronchial hypersensitivity induced by an exposure to the ovalbumin antigen, wherein the genes comprise any one of the nucleotide sequences of SEQ ID NOs: 1376 to 1515;

[17] the animal model according to [16], wherein the nonhuman vertebrate is a mouse;

[18] a method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease, which comprises the step of administering to a mouse any one of (i) to (iv):

(i) a polynucleotide comprising the nucleotide sequence constituting any one of the genes selected from the gene group according to (A) in [14];
(ii) a protein encoded by a polynucleotide comprising the nucleotide sequence constituting any one of the genes selected from the gene group according to [A] in [14];
(iii) an antisense nucleic acid of a polynucleotide comprising the nucleotide sequence constituting any one of the genes selected from the gene group according to (B) in [16], a ribozyme, or a polynucleotide that suppresses the expression of a gene through an RNAi (RNA interference) effect; and,
(iv) an antibody that binds to a protein encoded by a polynucleotide comprising the nucleotide sequence constituting any one of the genes selected from the gene group according to (B) in [16], or a fragment comprising an antigen-binding region thereof;

[19] an inducer that induces bronchial asthma in a mouse, wherein said inducer comprises as an active ingredient any one of (i) to (iv) in [18];

[20] a method of screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease comprising the steps of:

(1) administering a candidate compound to an animal subject,
(2) assaying the expression level of the marker gene in a biological sample obtained from the animal subject, and
(3) selecting a compound that decreases the expression level of a marker gene belonging to group (a) or (A), or a compound that increases the expression level of a marker gene belonging to group (b) or (B), as compared to that in a control with which the candidate compound has not been contacted,

wherein the marker gene is any one selected from the group consisting of (a) or (b) in [1], (A) in [14], and (B) in [16], or a gene functionally equivalent to said marker gene;

[21] a method of screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease comprising the steps of:

(1) contacting a candidate compound with a cell into which a vector has been introduced, wherein the vector comprises a transcriptional regulatory region of a marker gene and a reporter gene that is expressed under the control of the transcriptional regulatory region,
(2) measuring the activity of the reporter gene, and
(3) selecting a compound that decreases the expression level of the reporter gene when the marker gene belongs to group (a), or a compound that increases the expression level of the reporter gene when the marker gene belongs to group (b) , as compared to that in a control with which the candidate compound has not been contacted,

wherein the marker gene is any one selected from the group according to (a) or (b)in [1], or a gene functionally equivalent to the marker gene;

[22] a method of screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease comprising the steps of:

(1) contacting a candidate compound with a protein encoded by a marker gene,
(2) measuring the activity of the protein, and
(3) selecting a compound that decreases the activity when the marker gene belongs to group (a) , or a compound that increases the activity when the marker gene belongs to the group (b) , as compared to that in a control where the candidate compound has not been contacted,

wherein the marker gene is any one selected from the group according to (a) or (b)in [1], or a gene functionally equivalent to the marker gene;

[23] a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, which comprises as an active ingredient a compound obtainable by any one of the screening methods according to [7], [20], [21], and [22];

[24] a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, which comprises as an active ingredient a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, or a polynucleotide that suppresses the expression of the gene through an RNAi effect, wherein the marker gene is any one selected from the group according to (a) in [1] ;

[25] a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, which comprises as an active ingredient an antibody recognizing a protein encoded by a marker gene, wherein the marker gene is any one selected from the group according to (a) in [1];

[26] a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, which comprises as an active ingredient a marker gene, or a protein encoded by a marker gene, wherein the marker gene is any one selected from the group according to (b) in [1]; and

[27] a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilized to assay a marker gene, and wherein the marker gene comprises at least a single type of gene selected from group (a) and (b) in [1].

[0029] The present invention also relates to a method for treating bronchial asthma or a chronic obstructive pulmonary disease, which comprises the step of administering a compound obtainable by any one of the screening methods according to [7], [20], [21], and [22]. The present invention further relates to the use of a compound obtainable by any one of the screening methods according to [7], [20], [21], and [22] in producing pharmaceutical compositions to treat bronchial asthma or chronic obstructive pulmonary diseases.

[0030] In addition, the present invention relates to a method for treating bronchial asthma or chronic obstructive pulmonary disease, wherein the method comprises administering (i) or (ii) described below. Alternatively, the present invention relates to the use of (i) or (ii) described below, in producing pharmaceutical compositions for treating bronchial asthma or chronic obstructive pulmonary disease:

(i) a gene according to (a) described above or an antisense nucleic acid corresponding to a portion of the gene, a ribozyme, or a polynucleotide that suppresses the expression of the gene through an RNAi effect; and
(ii) an antibody recognizing a protein encoded by a gene according to (a) described above.

Furthermore, the present invention relates to a method for treating bronchial asthma or a chronic obstructive pulmonary disease, which comprises administering (iii) or (iv) described below. Alternatively, the present invention relates to the use of (iii) or (iv) described below, in producing pharmaceutical compositions to treat bronchial asthma or chronic obstructive pulmonary diseases:

(iii) a gene according to (b) described above; and
(iv) a protein encoded by a gene according to (b) described above.

BRIEF DESCRIPTION OF THE DRAWINGS

[0031]

Fig. 1 is a schematic diagram of the air interface (AI) method.
Fig. 2 is a schematic diagram showing the differences in the culture procedure between the air interface (AI) method and the immersed feeding (IMM) method.
Fig. 3 is a graph showing variations in the expression level of the pendrin gene during goblet cell differentiation when cultured by the AI method or the IMM method. The expression level (copy number/ng RNA) is indicated in the vertical axis, and the culture conditions and duration (in days) are indicated in the horizontal axis.
Fig. 4 is a graph showing the expression levels of the pendrin (PDS) gene in the lung of the mouse asthma model. The expression level (copy number/ng RNA) is indicated in the vertical axis, and the conditions used to treat mice and the number of individuals in each treated group are indicated in the horizontal axis.
naive: untreated group; S-sal: OVA antigen-sensitized, physiological saline-inhaled group; S-OVA: OVA antigen-sensitized, OVA antigen-inhaled group; Pred: OVA antigen-sensitized, OVA antigen-inhaled, Prednisolone-treated group
Fig. 5 shows micrographs (x 400) to determine the localization of the PDS mRNA in the lung tissues of the mouse asthma model using in situ hybridization.
Fig. 6 shows micrographs (x 400) of the lung tissues of the mouse asthma model. The tissues were subjected to hematoxylin-eosin (HE) staining, periodic acid-Schiff (PAS) staining, or Alcian Blue staining.
Figs 7-31 show the results of quantitative PCR assay analyses of genes whose expression levels varied in both humans and mice. The assays were carried out with ABI 7700 using cDNA of differentiated human goblet cells (human goblet cell differentiation model) or cDNA of the mouse OVA antigen-exposed bronchial hypersensitivity model. The vertical axis indicates the copy number of mRNA (copy number/ng total RNA). In the left panel, the horizontal axis indicates the culture conditions (AI method or IMM method) and duration (in days). In the right panel, the horizontal axis indicates the conditions used to treat mice and the number of antigen inhalation before collecting lung tissues.
naive: untreated group; S-sal: OVA antigen-sensitized, physiological saline-inhaled group;
S-OVA: OVA antigen-sensitized, OVA antigen-inhaled group; Pred: OVA antigen-sensitized, OVA antigen-inhaled, Prednisolone-treated group
Fig. 7 shows the assay result for the gene SCYB11. Likewise, the following Figures show the assay results for the respective genes. The symbols for the genes shown in the respective Figures are listed below.
Fig. 8: FBP1
Fig. 9: IL1RL1
Fig. 10: ALOX15
Fig. 11: ADAM8
Fig. 12: diubiquitin
Fig. 13: EPHX1
Fig. 14: RDC1
Fig. 15: IGFBP3
Fig. 16: IGFBP6
Fig. 17: S100A8
Fig. 18: CNTN1
Fig. 19: cig5
Fig. 20: SECTM1
Fig. 21: CP
Fig. 22: HEY1
Fig. 23: MGC14597
Fig. 24: UCP2
Fig. 25: STEAP
Fig. 26: LOC51297
Fig. 27: SLC34A2
Fig. 28: AQP5
Fig. 29: SLC26A4
Fig. 30: SCNN1B

DOCID: <EP_____1394274A2_I_>

Fig. 31: IL-13Ra2

Figs 32-69 show the results of quantitative PCR assays for genes whose expression levels varied in humans. The assays were carried out with ABI 7700 using cDNA of differentiated human goblet cells (human goblet cell differentiation model) or cDNA of the mouse OVA antigen-exposed bronchial hypersensitivity model. The vertical axis indicates the copy number of mRNA (copy number/ng total RNA). In the left panel, the horizontal axis indicates the culture conditions (the AI method or the IMM method) and duration (in days). In the right panel, the horizontal axis indicates the conditions used to treat mice and the number of antigen inhalation before collecting lung tissues.

naive: untreated group; S-sal: OVA antigen-sensitized, physiological saline-inhaled group;

S-OVA: OVA antigen-sensitized, OVA antigen-inhaled group; Pred: OVA antigen-sensitized, OVA antigen-inhaled, Prednisolone-treated group

Figs 32-69 (varies in human)

Fig. 32 shows the assay result for the gene NOS2A. Likewise, the following figures show the assay results for the respective genes. The symbols for the genes shown in the respective figures are listed below.

Fig. 33: ISG15 (only the result for the cDNA of human goblet cell differentiation model)
Fig. 34: CH25H (only the result for the cDNA of human goblet cell differentiation model)
Fig. 35: SERPINB4
Fig. 36: SERPINB2
Fig. 37: NCF2
Fig. 38: NOTCH3 (only the result for the cDNA of human goblet cell differentiation model)
Fig. 39: MDA5
Fig. 40: GBF5
Fig. 41: PRO1489 (only the result for the cDNA of human goblet cell differentiation model)
Fig. 42: MGC13102
Fig. 43: TGFB2
Fig. 44: DNAJA1
Fig. 45: SIAT1
Fig. 46: CISH
Fig. 47: AGR2 (only the result for the cDNA of human goblet cell differentiation model)
Fig. 48: MSMB (only the result for the cDNA of human goblet cell differentiation model)
Fig. 49: FLJ23516
Fig. 50: KCNMA1
Fig. 51: FLJ10298
Fig. 52: THBS1
Fig. 53: ABCC5
Fig. 54: SLC21A12 (only the result for the cDNA of human goblet cell differentiation model)
Fig. 55: SLC17A5 (only the result for the cDNA of human goblet cell differentiation model)
Fig. 56: connexin43
Fig. 57: BST2 (only the result for the cDNA of human goblet cell differentiation model)
Fig. 58: IFI9-27
Fig. 59: ICAM1
Fig. 60: periostin
Fig. 61: CDH-6
Fig. 62: DD96
Fig. 63: CTSC
Fig. 64: BENE (only the result for the cDNA of human goblet cell differentiation model)
Fig. 65: FLJ10261
Fig. 66: OAS2 (only the result for the cDNA of human goblet cell differentiation model)
Fig. 67: Odz2
Fig. 68: E48
Fig. 69: KRT16

DETAILED DESCRIPTION OF THE INVENTION

[0032] In the present invention, the term "allergic disease" is a general term used for a disease in which an allergic reaction is involved. More specifically, for a disease to be considered allergic, the allergen must be identified, a strong correlation between exposure to the allergen and the onset of a pathological change must be demonstrated, and it should have been proven that an immunological mechanism is behind the pathological change. Herein, the term "immunological mechanism" means that leukocytes show an immune response to allergen stimulation. Examples of al-

lergens are dust mite antigens, pollen antigens, etc.

[0033] Representative allergic diseases are bronchial asthma, allergic rhinitis, pollinosis, insect allergy, etc. Allergic diathesis is a genetic factor that is inherited from allergic parents to children. Familial allergic diseases are also called atopic diseases, and their causative factor that can be inherited is atopic diathesis.

[0034] Bronchial asthma is characterized by respiratory tract inflammation and varying degrees of airflow obstruction, and shows paroxysmal cough, wheezing, and difficulty in breathing. The degree of airflow obstruction ranges from mild to life-threatening obstructions. Such airway obstructions can be reversed at least in part either through natural healing or by treatment. Various types of cells infiltrating into the respiratory tract, such as eosinophils , T cells (Th2) , and mast cells, are involved in the inflammation and the damaging of the mucosal epithelium of the respiratory tract. The reversibility of airway obstruction tends to decrease in adult patients affected by the disease for a long time. In such cases, "remodelings" such as thickening of the basement membrane under the respiratory epithelium is often seen. In sensitive patients, respiratory remodeling accompanies bronchial hypersensitivity.

[0035] Herein, a gene that can be used as a marker for bronchial asthma is referred to as "marker gene". A protein comprising an amino acid sequence encoded by a marker gene is referred to as a "marker protein". Unless otherwise stated, the term "marker gene" is used as a terminology that refers to one or more arbitrary gene(s) selected from the genes according to (a) or (b):

(a) a group of genes whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13, and comprise any one of the nucleotide sequences of SEQ ID NOs: 25 to 310;

(b) a group of genes whose expression levels decrease when a respiratory epithelial cell is stimulated with interleukin-13 and comprise any one of the nucleotide sequences of SEQ ID NOs: 311 to 547;

[0036] The nucleotide sequences of the marker genes of the present invention or portions of the genes are known in the art. Some of the amino acid sequences encoded by the nucleotide sequences of the marker genes of the present invention have already been identified. The GenBank accession numbers for obtaining the data of partial nucleotide sequences of the marker genes, together with names of the marker genes, are listed below. In addition, the amino acid sequences of the marker proteins are shown in Tables 84-113.

[0037] When a partial nucleotide sequence of a marker gene has been identified, one skilled in the art can determine the full-length nucleotide sequence of the marker gene based on the information of the partial nucleotide sequence. Such a full-length nucleotide sequence can be obtained, for example, through *in-silico* cloning. Specifically, an EST nucleotide sequence constituting a portion of a marker gene (query sequence) is compared with massive amounts of expressed sequence tag (EST) information accumulated in public databases. Based on the comparison result, information of other ESTs that share a nucleotide sequence that coincides with the query sequence over a certain length is selected. The newly selected EST information is used as a new query sequence to gain other EST information, and this is repeated. A set of multiple ESTs sharing a partial nucleotide sequence can thus be obtained by this repetition. A set of ESTs is referred to as a "cluster". The nucleotide sequence of a gene of interest can be identified by assembling the nucleotide sequences of ESTs constituting a cluster into a single nucleotide sequence.

[0038] Furthermore, one skilled in the art can design PCR primers based on the nucleotide sequence determined through *in-silico* cloning. The presence of a gene comprising the determined nucleotide sequence can be verified by determining whether a gene fragment whose size is as expected is amplified by RT-PCR using such primers.

[0039] Alternatively, the result of *in-silico* cloning can be assessed by Northern blotting. Northern blotting is carried out using a probe designed based on the information of the determined nucleotide sequence. As a result, if a band that agrees with the above nucleotide sequence information is obtained, the presence of a gene comprising the determined nucleotide sequence can be verified.

[0040] A gene of interest can be isolated empirically, in addition to *in-silico* cloning. First, a cDNA clone that provided nucleotide sequence information deposited as an EST is obtained. Then, the entire nucleotide sequences of the cDNA in that clone are determined. As a result, it may be possible to determine the full-length sequence of the cDNA. At least it is possible to determine a longer nucleotide sequence. The length of the cDNA in the clone can be pre-determined empirically when the vector structure is known.

[0041] Even if the clone that provided nucleotide sequence information of an EST is unavailable, there is a method known in the art by which an unknown part of a nucleotide sequence of a gene can be obtained based on a partial nucleotide sequence of the gene. For example, in some cases, a longer nucleotide sequence can be identified by screening a cDNA library using an EST as a probe. When a cDNA library comprising many full-length cDNA is used in the screening, a full-length cDNA clone can be readily isolated. For example, a cDNA library synthesized by the oligo-capping method is known to contain many full-length cDNA.

[0042] Furthermore, there is a technique known in the art to synthesize an unknown portion of a gene, based on the information of a partial nucleotide sequence of the gene. For example, RACE is a representative technique for isolating a gene comprising an unknown nucleotide sequence. In RACE, an oligonucleotide linker is artificially ligated to one

end of a cDNA. The oligonucleotide linker consists of a known nucleotide sequence. Thus, PCR primers can be designed based on the information of a portion whose nucleotide sequence is already known as an EST and the nucleotide sequence of the oligonucleotide linker. The nucleotide sequence of the unknown region can be synthesized specifically by PCR using the primers designed as described above.

[0043] The method of testing for allergic diseases of the present invention comprises measuring the expression level of each marker gene in a biological sample from a subject and comparing the level with that of the marker gene in a control biological sample. When the marker gene is one of the genes according to (a) described above and the expression level is higher than that in the control, the subject is judged to be affected with bronchial asthma or a chronic obstructive pulmonary disease. Alternatively, when the marker gene is one of the genes according to (b) described above and the expression level is lower than that in the control, the subject is judged to be affected with bronchial asthma or a chronic obstructive pulmonary disease. In the present invention, a respiratory epithelial cell which has not been stimulated with IL-13, can be used as a control. Preferably, the control respiratory epithelial cell has been cultured by the AI method.

[0044] The standard value for the control may be pre-determined by measuring the expression level of the marker gene in the control, in order to compare the expression levels. Typically, for example, the standard value is determined based on the expression level of the above-mentioned marker gene in the control. For example, the permissible range is taken as ±2S.D. based on the standard value. A technique for determining the permissible range and the standard value based on a measured value for the marker gene is known in the art. Once the standard value is determined, the testing method of the present invention may be performed by measuring only the expression level in a biological sample from a subject and comparing the value with the determined standard value for the control.

[0045] When the marker gene is one of the genes according to (a) described above and the expression level in a subject is higher than the permissible range in comparison to that in the control, the subject is judged to be affected with bronchial asthma or a chronic obstructive pulmonary disease. Likewise, when the marker gene is one of the genes according to (b) described above and the expression level in a subject is lower than the permissible range in comparison to that in the control, the subject is judged to be affected with bronchial asthma or a chronic obstructive pulmonary disease. When the expression level of the marker gene falls within the permissible range, the subject is unlikely to be affected with bronchial asthma or a chronic obstructive pulmonary disease.

[0046] In this invention, expression levels of marker genes include transcription of the marker genes to mRNA, and translation into proteins. Therefore, the method of testing for bronchial asthma or a chronic obstructive pulmonary disease of this invention is performed based on a comparison of the intensity of expression of mRNA corresponding to the marker genes, or the expression level of proteins encoded by the marker genes.

[0047] The measurement of the expression levels of marker genes in the testing for bronchial asthma or a chronic obstructive pulmonary disease of this invention can be carried out according to known gene analysis methods. Specifically, one can use, for example, a hybridization technique using nucleic acids that hybridize to these genes as probes, or a gene amplification technique using DNA that hybridize to the marker genes of this invention as primers.

[0048] The probes or primers used for the testing of this invention can be designed based on the nucleotide sequences of the marker genes. The nucleotide sequences of the marker genes and a portion of amino acid sequences encoded by the genes are known. The GenBank accession numbers for the known nucleotide sequences of the respective marker genes of the present invention are shown below in Tables 3-19 (genes showing increased expression) and Tables 20-36 (genes showing decreased expression). When a gene has a number beginning with NM in the column of RefSeq in Tables, the full-length nucleotide sequence of the gene is known in the art. When a gene does not have a number beginning with NM in the column of RefSeq, a partial nucleotide sequence can be obtained based on the GenBank Accession number of the gene. As described above, the full-length nucleotide sequence of a gene can be obtained based on the information of a known partial nucleotide sequence. In addition, with respect to some of the marker genes of the present invention, the nucleotide sequences and the amino acid sequences encoded by them are shown in the Tables.

[0049] Genes of higher animals generally accompany polymorphism in a high frequency. There are also many molecules that produce isoforms comprising mutually different amino acid sequences during the splicing process. Any gene associated with bronchial asthma or a chronic obstructive pulmonary disease that has an activity similar to that of a marker gene is included in the marker genes of the present invention, even if it has nucleotide sequence differences due to polymorphism or being an isoform.

[0050] Herein, the marker genes include homologs of other species in addition to humans. Thus, unless otherwise specified, the expression "marker gene in a species other than human" refers to a homolog of the marker gene unique to the species or a foreign marker gene which has been introduced into an individual.

[0051] As used herein, the expression "homolog of a human marker gene" refers to a gene derived from a species other than a human, which can hybridize to the human marker gene as a probe under stringent conditions. Stringent conditions typically mean hybridization in 4x SSC at 65°C followed by washing with 0.1x SSC at 65°C for 1 hour. Temperature conditions for hybridization and washing that greatly influence stringency can be adjusted according to

the melting temperature (Tm). Tm varies with the ratio of constitutive nucleotides in the hybridizing base pairs, and the composition of the hybridization solution (concentrations of salts, formamide, and sodium dodecyl sulfate). Therefore, considering these conditions, one skilled in the art can select an appropriate condition to produce an equal stringency experimentally or empirically.

[0052] An example of a homolog of the marker genes of the present invention, which is derived from another species, is the mouse homolog. Using the mouse model of bronchial hypersensitivity, the present inventors confirmed that the mouse genes according to (A) or (B) exhibit variation patterns of expression levels similar to that of human marker genes. This finding supports the fact that there is a close relationship between the human marker genes identified in the present invention and the allergic responses of tissues in the respiratory tract. This finding also supports the fact that homologs of various species can be used as marker genes of the present invention.

[0053] A polynucleotide comprising the nucleotide sequence of a marker gene or a nucleotide sequence that is complementary to the complementary strand of the nucleotide sequence of a marker gene and has at least 15 nucleotides , can be used as a primer or probe. Herein, the expression "complementary strand" means one strand of a double stranded DNA with respect to the other strand and which is composed of A: T (U for RNA) and G:C base pairs. In addition, "complementary" means not only those that are completely complementary to a region of at least 15 continuous nucleotides, but also those that have a nucleotide sequence homology of at least 70%, preferably at least 80%, more preferably 90%, and even more preferably 95% or higher. The degree of homology between nucleotide sequences can be determined by an algorithm, BLAST, etc.

[0054] Such polynucleotides are useful as a probe to detect a marker gene, or as a primer to amplify a marker gene. When used as a primer, the polynucleotide comprises usually 15 bp to 100 bp, preferably 15 bp to 35 bp of nucleotides. When used as a probe, a DNA comprises the whole nucleotide sequence of the marker gene (or the complementary strand thereof) , or a partial sequence thereof that has at least 15-bp nucleotides. When used as a primer, the 3' region must be complementary to the marker gene, while the 5' region can be linked to a restriction enzyme-recognition sequence or a tag.

[0055] "Polynucleotides" in the present invention may be either DNA or RNA. These polynucleotides may be either synthetic or naturally-occurring. Also, DNA used as a probe for hybridization is usually labeled. Examples of labeling methods are those as described below. Herein, the term "oligonucleotide" means a polynucleotide with a relatively low degree of polymerization. Oligonucleotides are included in polynucleotides. The labeling methods are as follows:

- nick translation labeling using DNA polymerase I;
- end labeling using polynucleotide kinase;
- fill-in end labeling using Klenow fragment (Berger, SL, Kimmel, AR. (1987) Guide to Molecular Cloning Techniques, Method in Enzymology, Academic Press; Hames, BD, Higgins, SJ. (1985) Genes Probes: A Practical Approach. IRL Press; Sambrook, J., Fritsch, EF, Maniatis, T. (1989) Molecular Cloning: a Laboratory Manual, 2nd Edn. Cold Spring Harbor Laboratory Press);
- transcription labeling using RNA polymerase (Melton, DA, Krieg, PA, Rebagkiati, MR, Maniatis, T, Zinn, K, Green, MR. (1984) Nucleic Acid Res., 12, 7035-7056); and
- non-isotopic labeling of DNA by incorporating modified nucleotides (Kricka, LJ. (1992) Non-isotopic DNA Probing Techniques. Academic Press).

[0056] Tests for bronchial asthma or a chronic obstructive pulmonary disease using hybridization techniques, can be performed using, for example, Northern hybridization, dot blot hybridization, or the DNA microarray technique. Furthermore, gene amplification techniques, such as the RT-PCR method may be used. By using the PCR amplification monitoring method during the gene amplification step in RT-PCR, one can achieve a more quantitative analysis of the expression of a marker gene of the present invention.

[0057] In the PCR gene amplification monitoring method, the detection target (DNA or reverse transcript of RNA) is hybridized to probes that are labeled with a fluorescent dye and a quencher which absorbs the fluorescence. When the PCR proceeds and Taq polymerase degrades the probe with its 5'-3' exonuclease activity, the fluorescent dye and the quencher draw away from each other and the fluorescence is detected. The fluorescence is detected in real time. By simultaneously measuring a standard sample in which the copy number of a target is known, it is possible to determine the copy number of the target in the subject sample with the cycle number where PCR amplification is linear (Holland, P. M. et al., 1991, Proc. Natl. Acad. Sci. USA 88: 7276-7280; Livak, K. J. et al. , 1995, PCR Methods and Applications 4(6): 357-362; Heid, C. A. et al., 1996, Genome Research 6: 986-994; Gibson, E. M. U. et al., 1996, Genome Research 6: 995-1001). For the PCR amplification monitoring method, for example, ABI PRISM7700 (Applied Biosystems) may be used.

[0058] The method of testing for bronchial asthma or a chronic obstructive pulmonary disease of the present invention can be also carried out by detecting a protein encoded by a marker gene. Hereinafter, a protein encoded by a marker gene is described as a "marker protein". For such test methods, for example, the Western blotting method, the immu-

noprecipitation method, and the ELISA method may be employed using an antibody that binds to each marker protein.

[0059] Antibodies used in the detection that bind to the marker protein may be produced by techniques known to those skilled in the art. Antibodies used in the present invention may be polyclonal or monoclonal (Milstein, C. et al., 1983, Nature 305 (5934): 537-40). For example, a polyclonal antibody against a marker protein may be produced by collecting blood from mammals sensitized with the antigen, and separating the serum from this blood using known methods. As a polyclonal antibody, serum containing a polyclonal antibody may be used. If necessary, a fraction containing the polyclonal antibody can be further isolated from this serum. Also, a monoclonal antibody may be obtained by isolating immune cells from mammals sensitized with the antigen, fusing these cells with myeloma cells and such, cloning the resulting hybridomas, and then collecting the antibody from the hybridoma culture.

[0060] In order to detect a marker protein, such an antibody may be appropriately labeled. Alternatively, instead of labeling the antibody, a substance that specifically binds to the antibody, for example, protein A or protein G, may be labeled to detect the marker protein indirectly. More specifically, such a detection method includes the ELISA method.

[0061] A protein or a partial peptide thereof used as an antigen may be obtained, for example, by inserting a marker gene or a portion thereof into an expression vector, introducing the construct into an appropriate host cell to produce a transformant, culturing the transformant to express the recombinant protein, and purifying the expressed recombinant protein from the culture or the culture supernatant. Alternatively, the amino acid sequence encoded by a gene or an oligopeptide comprising a portion of the amino acid sequence encoded by a full-length cDNA are chemically synthesized to be used as an immunogen.

[0062] Furthermore, in the present invention, a test for an allergic disease can be performed using as an index not only the expression level of a marker gene but also the activity of a marker protein in a biological sample. Activity of a marker protein means the biological activity intrinsic to the protein. Typical methods for measuring the activity of each protein are described below.

[Protease]

[0063] A protease sample is electrophoresed under a non-reducing condition in an SDS polyacrylamide gel copolymerized with a substrate such as gelatin. After electrophoresis, the gel is allowed to stand still in an appropriate buffer at 37°C for 16 hours. The gel is stained with Coomassie Brilliant Blue R250 after 16 hours. The protease activity can be assessed by verifying that the electrophoretic position corresponding to the protease is not stained on the gel, i.e., gelatin at that position has been hydrolyzed.

Chen, J. M. et al., J. Biol. Chem. 266, 5113-5121 (1991)

[Protease inhibitor]

[0064] A protease inhibitor is electrophoresed under a non-reducing condition in an SDS polyacrylamide gel copolymerized with a protease substrate such as gelatin. After electrophoresis, the gel is allowed to stand still in an appropriate buffer containing a protease at 37°C for 16 hours. After 16 hours, the gel is stained with Coomassie Brilliant Blue R250. The activity of the protease inhibitor can be assessed by verifying that the electrophoretic position corresponding to the protease inhibitor is not stained on the gel, i.e., gelatin has not been hydrolyzed at that position.

Greene J. et al., J. Biol. Chem. 271, 30375-30380 (1996)

[Transcription factor]

[0065] A transcription factor is incubated at room temperature with a double-stranded oligo DNA, which has been labeled with ^{32}p or such and contains a target sequence of the transcription factor. The incubation allows the transcription factor to bind to the oligo DNA. After incubation, the sample is electrophoresed in a native polyacrylamide gel without SDS. The mobility of the labeled oligo DNA is determined using the radioactivity of ^{32}P or such as an index. When the transcription factor has the activity of binding to the oligo DNA, the mobility of the labeled oligo DNA decreases and thus the band shifts to a higher-molecular-weight position. The binding specificity for the target sequence can be assessed by verifying that an excess amount of non-labeled double-stranded oligo DNA inhibits the binding between the transcription factor and the labeled oligo DNA.

[0066] In addition, the ability to activate transcription by a transcription factor can be estimated by a procedure which comprises the steps of: co-introducing into cells of a cell line such as HeLa or HEK293, an expression vector comprising a reporter gene such as chloramphenicol acetyltransferase (CAT) downstream of a target sequence and another expression vector comprising the transcription factor gene downstream of a promoter from human cytomegalovirus (CMV) , and after 48 hours, preparing a cell lysate and determining the expression level of CAT in the lysate.

Zhao F. et al., J. Biol. Chem. 276, 40755-40760 (2001)

[Kinase]

[0067] A kinase is added to a buffer (20 mM HEPES, pH7.5, 10 mM $MgCl_2$, 2 mM $MnCl_2$, 2 mM dithiothreitol, and 25 μM ATP) containing myelin basic protein as a substrate, and then [γ-^{32}P]ATP is added thereto. The resulting mixture is incubated at 37°C for 10 minutes. After 10 minutes, Laemmli buffer is added to stop the reaction, and the reaction solution is subjected to SDS polyacrylamide gel electrophoresis. After electrophoresis, the gel is dried and the radioactivity of the phosphorylated myelin basic protein is detected on X-ray film.

Park SY. et al., J. Biol. Chem. 275, 19768-19777 (2000)

[Phosphatase]

[0068] A phosphatase is added to a buffer (25 mM MES (pH 5.5) , 1.6 mM dithiothreitol, and 10 mM pNPP) containing p-nitrophenyl phosphate (pNPP) as a substrate. The resulting mixture is incubated at 37°C for 30 minutes. After 30 minutes, 1N NaOH is added to stop the reaction, and the absorbance at 405 nm, a result of pNpp hydrolysis, is measured.

Aoyama K. et al., J. Biol. Chem. 276, 27575-27583 (2001)

[Chemokine and chemokine receptor]

[0069] Cells overexpressing a chemokine receptor are suspended in Hank's balanced salt solution containing the calcium-sensitive fluorescent dye fura-2. The cells are stimulated with the chemokine. An increase in the intracellular calcium level that resulted from the chemokine stimulation is measured with a fluorescence detector such as LS50B (Perkin Elmer).

Zhou N. et al., J. Biol. Chem. 276, 42826-42833 (2001)

[Cytokine and cytokine receptor]

[0070] Cells expressing a cytokine receptor are stimulated with a cytokine. The resulting cell proliferation is assessed by thymidine uptake.

[0071] Alternatively, it is possible to assess the cytokine-mediated activation of a transcription factor downstream of the cytokine receptor based on the expression of a reporter gene such as luciferase.

Piek E. et al., J. Biol. Chem. 276, 19945-19953 (2001)

[Ion channel]

[0072] An ion channel-containing cell membrane is attached to the open end, the area of which is a few μm^2, of a glass pipette. The ion channel activity can be determined by the patch-clamp method which comprises measuring the electric current passing through the channel when a potential difference is generated between the inside and outside of the pipette.

Hamill, O. P. et al., Pfluegers Arch. 391, 85-100 (1981)

[Cell adhesion molecule]

[0073] Cells expressing an adhesion molecule on the cell surface are incubated in a plate coated with the ligand of the molecule. The number of cells adhering to the plate is determined.

Fujiwara H. et al., J. Biol. Chem. 276, 17550-17558 (2001)

[Extracellular matrix protein]

[0074] A suspension of cells expressing a receptor of an extracellular matrix protein such as integrin, is added to a plate coated with an extracellular matrix protein. The plate is incubated at 37°C for 1 hour. After incubation, the cells are fixed and a DNA-binding fluorescent dye such as Hoechst 33342, is added thereto. After the reaction, the fluorescence intensity is determined using a fluorometer. The number of adhered cells quantified based on the fluorescence intensity is used to assess the activity of the extracellular matrix protein.

Miyazaki K. et al., Proc. Natl. Acad. Sci. U. S. A. 90, 11767 (1993)

[0075] Normally, a biological material collected from a subject is used as a sample in the testing method of the present invention. A preferred biological sample is blood. Blood samples include whole blood, and plasma and serum prepared from whole blood. The biological sample of the present invention includes sputum, secretions from the nasal mucous

membrane, bronchoalveolar lavage fluid, exfoliated airway epithelial cells, in addition to blood. Methods for collecting biological samples are known in the art.

[0076] When the biological sample is cells such as respiratory tract epithelial cells, samples for immunological measurements of the aforementioned proteins can be made by preparing a lysate. Alternatively, samples for measuring mRNA corresponding to the aforementioned genes can be prepared by extracting mRNA from this lysate. A commercially available kit is useful when extracting a lysate or mRNA from a biological sample. Alternatively, biological samples in the liquid form such as blood, nasal mucous secretions, and bronchoalveolar lavage fluids can be made into samples for measurement of proteins and genes by diluting with a buffer and such, as necessary.

[0077] A lysate prepared from an above-mentioned biological sample can be used as a sample in immunological assays for marker proteins. Alternatively, mRNA extracted from the lysate can be used as a sample in assays for mRNA corresponding to marker genes. A commercially available kit can be used to prepare a lysate or to extract mRNA from a biological sample. When a marker protein is secreted into blood, the expression level of the encoding gene can be compared by determining the amount of the protein of interest in a sample of a subject's body fluid such as blood or serum. The sample can be diluted with a buffer or such, as required, to be used in the method of the present invention.

[0078] When mRNA is measured, the measured value of the expression levels of marker genes in the present invention can be corrected by known methods. As a result of correction, variations in gene expression levels in cells can be compared. Based on the measured values of the expression levels of genes that do not show great variations in each cell in the above biological samples (for example, housekeeping genes), the correction of the measured values is done by correcting the measured values of the expression levels of marker genes in this invention. Genes whose expression level does not greatly vary include β-actin and GAPDH.

[0079] Furthermore, the present invention provides reagents for the testing methods of the present invention. Specifically, the present invention relates to a reagent for testing bronchial asthma or a chronic obstructive pulmonary disease, which comprise a polynucleotide comprising the nucleotide sequence of a marker gene, or an oligonucleotide having at least 15 nucleotides and comprising a nucleotide sequence complementary to the complementary strand of the nucleotide sequence of the marker gene. The present invention also relates to a reagent for testing bronchial asthma or a chronic obstructive pulmonary disease, which comprises an antibody recognizing a marker protein.

[0080] The oligonucleotide or antibody constituting the reagents of the present invention can be pre-labeled with an appropriate labeling substance depending on the assay. Alternatively, the oligonucleotide or antibody constituting the reagents of the present invention can be pre-immobilized on an appropriate support depending on the assay. Furthermore, the reagents of the present invention can be prepared as test kits in combination with an additive necessary for the testing and storage, in addition to the oligonucleotide or antibody described above. Exemplary additives constituting such a kit are listed below. If required, these may be added in advance. A preservative may also be added to each.

[0081] A buffer for diluting the reagent or biological sample;
positive control;
negative control;
substrate to be used for detecting a label;
reaction vessel; and
instruction manual describing assay protocols.

[0082] The expression level of a marker gene of the present invention has been confirmed to change in respiratory epithelial cells upon IL-13 stimulation in comparison to that in non-stimulated respiratory epithelial cells. Thus, bronchial asthma or a chronic obstructive pulmonary disease can be tested using as an index the expression level of a marker gene.

[0083] Tests for bronchial asthma or a chronic obstructive pulmonary disease according to the present invention include, for example, the following. Even if a patient is not diagnosed as being affected with bronchial asthma or a chronic obstructive pulmonary disease in a routine test in spite of symptoms suggesting these diseases, whether or not such a patient is suffering from bronchial asthma or a chronic obstructive pulmonary disease can be easily determined by performing a test according to the present invention. More specifically, when the marker gene is one of the genes according to (a) mentioned above, an increase in the expression level of the marker gene in a patient whose symptoms suggest bronchial asthma or chronic obstructive pulmonary disease, implies that the symptoms are caused by bronchial asthma or a chronic obstructive pulmonary disease. Alternatively, when the marker gene is one of the genes according to (b) mentioned above, likewise, a decrease in the expression level of a marker gene in a patient whose symptoms suggest bronchial asthma or a chronic obstructive pulmonary disease, implies that the symptoms are caused by bronchial asthma or a chronic obstructive pulmonary disease.

[0084] In addition, the present invention facilitates tests to determine whether bronchial asthma or a chronic obstructive pulmonary disease is improving in a patient. In other words, the present invention can be used to judge the therapeutic effect on bronchial asthma or a chronic obstructive pulmonary disease. Furthermore, when the marker gene is one of the genes according to (a), an increase in the expression level of the marker gene in a patient, who has been diagnosed as being affected by bronchial asthma or a chronic obstructive pulmonary disease, implies that the disease

has progressed more. Alternatively, when the marker gene is one of the genes according to (b) , likewise a decrease in the expression level of the marker gene in a patient, who has been diagnosed as being affected by bronchial asthma or a chronic obstructive pulmonary disease, implies that the disease has progressed more.

[0085] Furthermore, the severity of bronchial asthma or a chronic obstructive pulmonary disease may also be determined based on the difference in expression levels. In other words, when the marker gene is one of the genes according to (a), the degree of increase in the expression level of the marker gene is correlated with the severity of bronchial asthma or chronic obstructive pulmonary disease. Alternatively, when the marker gene is one of the genes according to (b) , the degree of decrease in the expression level of the marker gene is correlated with the severity of bronchial asthma or chronic obstructive pulmonary disease.

[0086] The present invention also relates to animal models for bronchial asthma or chronic obstructive pulmonary disease, comprising a nonhuman transgenic animal in which the expression level of a marker gene according to (a) or a gene functionally equivalent to the marker gene has been elevated in the respiratory epithelium.

[0087] The present invention revealed that stimulation with IL-13 increased the expression level of a marker gene according to (a) in respiratory epithelial cells. Thus, an animal in which the expression level of a marker gene according to (a) or a gene functionally equivalent to the marker gene in respiratory epithelial cells has been artificially increased, can be used as an animal model for bronchial asthma or chronic obstructive pulmonary diseases.

[0088] The present invention also relates to an animal model for bronchial asthma or chronic obstructive pulmonary disease, which is a nonhuman transgenic animal in which the expression level of a marker gene according to (b) , or a gene functionally equivalent to the marker gene, has been decreased in respiratory epithelial cells.

[0089] The present invention revealed that stimulation with IL-13 decreased the expression level of a marker gene according to (b) in respiratory epithelial cells. Thus, an animal in which the expression level of a marker gene according to (b) or a gene functionally equivalent to the marker gene in respiratory epithelial cells has been artificially decreased can be used as an animal model for bronchial asthma or chronic obstructive pulmonary disease.

[0090] A "functionally equivalent gene" as used in this invention is a gene that encodes a protein having an activity similar to a known activity of a protein encoded by the marker gene. A representative example of a functionally equivalent gene includes a counterpart of a marker gene of a subject animal, which is intrinsic to the animal.

[0091] For example, genes according to group (A) and group (B) described above are functionally equivalent mouse genes. The genes according to group (A) and group (B) described above are used as preferred marker genes in performing the screenings according to the present invention using mice.

[0092] In addition, the present invention identified the mouse counterpart genes of the marker genes according to (a) and (b). Such counterpart genes are shown in (A) and (B) , respectively. These counterparts are genes whose expression levels in respiratory epithelial cells showed a twofold or more difference between the mouse model for bronchial asthma and normal mice. Thus, an animal model for bronchial asthma can be created by controlling the expression level of a counterpart gene or administering a counterpart gene. Namely, the present invention relates to a method for creating an animal model for bronchial asthma or a chronic obstructive pulmonary disease by controlling the expression level of a gene selected from the group of genes according to (A) or (B). Alternatively, the present invention relates to a method for creating an animal model for bronchial asthma or a chronic obstructive pulmonary disease by administering the protein encoded by a gene selected from the group of genes according to (A) or (B) , or administering an antibody against the protein.

[0093] First, similarly to the group of genes according to (a), the group of genes according to (A) can induce bronchial asthma or a chronic obstructive pulmonary disease by the increase in their expression levels. Alternatively, an animal model for bronchial asthma or chronic obstructive pulmonary disease can be created by introducing a gene selected from such groups of genes, or by administering a protein encoded by such a gene. Such counterpart genes or proteins are preferably introduced/administered to mice, because they derive from mice.

[0094] In addition, similarly to the group of genes according to (b), the group of genes according to (B) can induce bronchial asthma or chronic obstructive pulmonary disease by the suppression of their expression levels. Alternatively, bronchial asthma or chronic obstructive pulmonary disease can be induced by suppressing the expression of a gene selected from such groups of genes or the activity of a protein encoded by such a gene. An antisense nucleic acid, a ribozyme, or an RNAi can be used to suppress the expression. The activity of a protein can be controlled effectively by administering a substance that inhibits the activity, such as an antibody. Namely, in an animal inherently having a gene selected from the group of genes according to (B) , i.e. , mice, bronchial asthma or chronic obstructive pulmonary disease is induced by administering such a substance.

[0095] The animal model for bronchial asthma or chronic obstructive pulmonary disease is useful for detecting physiological changes due to bronchial asthma or chronic obstructive pulmonary disease. Furthermore, the use of the animal model for bronchial asthma or chronic obstructive pulmonary disease to reveal additional functions of marker genes and evaluate drugs whose targets are the marker genes, also have a great significance.

[0096] In addition, the animal model for bronchial asthma or chronic obstructive pulmonary disease of the present invention can be used to elucidate the mechanism underlying bronchial asthma or chronic obstructive pulmonary dis-

ease and also to test the safety of compounds obtained by screening. For example, when an animal model for bronchial asthma or chronic obstructive pulmonary disease according to the present invention develops the symptoms of asthma or chronic obstructive pulmonary disease, or when a measured value involved in a certain allergic disease alters in the animal, a screening system can be constructed to explore compounds having activity to alleviate the disease.

[0097] As used herein, the expression "an increase in the expression level" refers to any one of the following: where a marker gene introduced as a foreign gene is expressed artificially; where the transcription of a marker gene intrinsic to the subject animal and the translation thereof into the protein are enhanced; or where the hydrolysis of the protein, which is the translation product, is suppressed.

[0098] As used herein, the expression "a decrease in the expression level" refers to either the state in which the transcription of a marker gene of the subject animal and the translation thereof into the protein are inhibited, or the state in which the hydrolysis of the protein, which is the translation product, is enhanced. The expression level of a gene can be determined, for example, by a difference in signal intensity on a DNA chip as shown below in the Example. Furthermore, the activity of the translation product -the protein- can be determined by comparing with that in the normal state.

[0099] Representative transgenic animals include: animals to which a marker gene has been introduced and expressed artificially; marker gene knockout animals; and knock-in animals in which another gene has been substituted for a marker gene. A transgenic animal, into which an antisense nucleic acid of a marker gene, a ribozyme, a polynucleotide having an RNAi effect, or a DNA functioning as a decoy nucleic acid or such has been introduced, can be used as the transgenic animal of the present invention. Such transgenic animals also include, for example, animals in which the activity of a marker protein has been enhanced or suppressed by introducing a mutation(s) into the coding region of the gene, or the amino acid sequence has been modified to become resistant or susceptible to hydrolysis. Mutations in an amino acid sequence include substitutions, deletions, insertions, and additions. In addition, the expression itself of a marker gene of the present invention can be controlled by introducing a mutation (s) into the transcriptional regulatory region of the gene.

[0100] An amino acid substitution is preferably a "conservative amino acid substitution" -a mutation of an amino acid into a different amino acid that conserves the properties of the amino acid side-chain-. A "conservative amino acid substitution" is a replacement of one amino acid residue belonging to one of the following groups having a chemically similar side chain with another amino acid in the same group. Groups of amino acid residues having similar side chains have been defined in the art. These groups include amino acids with basic side chains (e.g., lysine, arginine, histidine) , acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g. , alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine).

[0101] The number of amino acids that are mutated is not particularly restricted, as long as the activity is maintained. Normally, it is within 50 amino acids, preferably within 30 amino acids, more preferably within 10 amino acids, and even more preferably within 3 amino acids. The site of mutation may be any site, as long as the activity is maintained.

[0102] Methods for obtaining transgenic animals by targeting a particular gene are known. That is, a transgenic animal can be obtained by any of the following methods: mixing a gene and ovum and treating with calcium phosphate; introducing a gene directly into the nucleus of an oocyte in a pronuclei with a micropipette under a phase contrast microscope (microinjection method, US Patent No. 4873191) ; or using embryonic stem cells (ES cells). Furthermore, a method for infecting ovum with a gene-inserted retroviral vector, the sperm vector technique for transducing a gene into ovum via sperm, or such, have also been developed. The sperm vector technique is a gene recombination technique for introducing a foreign gene by fertilizing ovum with sperm after a foreign gene has been incorporated into sperm by adhesion or the electroporation method, etc. (M. Lavitrano, et al., Cell, 57, 717, 1989).

[0103] When a promoter whose transcription activity is controlled by a substance such as an appropriate drug is used in the expression vector, the expression level of a foreign marker gene can be regulated by administering the substance to the transgenic animal.

[0104] Transgenic animals used as the animal model for bronchial asthma or chronic obstructive pulmonary disease of the present invention can be produced using all vertebrates except humans. More specifically, transgenic animals having various transgenes or modified gene expression levels are being produced using vertebrates such as mice, rats, rabbits, miniature pigs, goats, sheep, monkeys, dogs, cats, or cattle.

[0105] In addition, the present invention relates to screening methods for candidate compounds for therapeutic agents to treat bronchial asthma or chronic obstructive pulmonary disease. According to the present invention, a marker gene is selected from the group according to the above (a) or (b). When the gene is selected from the group according to (a) , the expression level is significantly elevated in respiratory epithelial cells stimulated with IL-13 in comparison with unstimulated respiratory epithelial cells. When the gene is selected from the group according to (b) , the expression level is significantly decreased in respiratory epithelial cells stimulated with IL-13 in comparison with unstimulated respiratory epithelial cells.

[0106] Thus, when the marker gene belongs to group (a), a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease can be obtained by selecting a compound capable of decreasing the expression level of the marker gene. On the other hand, when the marker gene belongs to group (b) , a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease can be obtained by selecting a compound capable of increasing the expression level of the marker gene.

[0107] As used herein, the expression "a compound that increases the expression level of a gene" refers to a compound that promotes any one of the steps of gene transcription, gene translation, or expression of a protein activity. On the other hand, the expression "a compound that decreases the expression level of a gene", as used herein, refers to a compound that inhibits any one of these steps.

[0108] A method of screening for a therapeutic agent for an allergic disease of this invention can be carried out either *in vivo* or *in vitro.* This screening method can be performed, for example, according to the steps as described below:

(1) administering a candidate compound to an animal subject;
(2) measuring the expression level of a marker gene in a biological sample from the animal subject;
(3) selecting a compound that decreases the expression level of a marker gene belonging to group (a) , or a compound that increases the expression level of a marker gene belonging to group (b) , as compared to that in a control with which the candidate compound has not been contacted;

[0109] In the screening methods of the present invention, a gene functionally equivalent to any one of the genes selected from the group according to (a) or (b) described above, can be used as a marker gene. A representative example of a functionally equivalent gene includes a counterpart marker gene of a subject animal, which is intrinsic to the animal.

[0110] An animal used in the screening method of the present invention includes, for example, an animal model for bronchial asthma known in the art. For example, the animal model for ovalbumin (hereinafter abbreviated as "OVA") antigen-exposed bronchial hypersensitivity has been reported as an animal model for bronchial asthma. Bronchial hypersensitivity can be induced as follows: 50 μg OVA and 1 mg aluminum hydroxide as an adjuvant are injected into the peritoneal cavity of Balb/c mice (male, seven-week old), and after 10 days, the mice are sensitized with OVA by the same procedure. Then, after 10 days, 1% OVA is given to the mice by inhalation using Ultra-nebulizer model UN701 (Azwell, Inc.) for 30 minutes every four days three times in total. The enhanced bronchial hypersensitivity is monitored by detecting respiratory constriction caused by acetylcholine (6.25-2000 mg/kg) using a respirator (model 131, New England Medical Instruments Inc.) 24 hours after the final antigen inhalation (Nagai H. et al, Int Arch Allergy Immunol; 108: 189-195, 1995).

[0111] Furthermore, an animal model for chronic obstructive pulmonary disease is also known in the art. The animal model can be created using mice, rats, rabbits, miniature pigs, dogs, horses, etc. For example, an animal model for chronic obstructive pulmonary disease, which develops symptoms such as pulmonary emphysema, can be created by giving erastase to a New Zealand white rabbit three times by inhalation (Brenner M. et al., Chest, 121, 201-209, 2002). The screening according to the present invention can be practiced by administering a candidate compound to such an animal model and then monitoring variations in the expression level of a marker gene of the present invention.

[0112] A screening method using an animal model typically comprises monitoring the expression level of a marker gene that is inherently contained in the animal model. Thus, for example, the expression level of the mouse homolog of a marker gene is measured when the screening method uses a mouse model. Mouse genes according to (A) are genes whose expression levels are elevated in respiratory tissues of an OVA antigen-exposed bronchial hypersensitivity mouse model. On the other hand, mouse genes according to (B) are genes whose expression levels are decreased in respiratory tissue of the same mouse model. These mouse homolog genes can be used as marker genes in the screening methods of the present invention.

[0113] In addition to mouse homologs, one skilled in the art can identify similar homologs of various animal species based on the disclosure of the present invention. For example, various genes (or proteins) exhibiting a high homology to the nucleotide sequence or the amino acid sequence of a human marker gene or a mouse homolog can be identified by using homology searches. Alternatively, such homologs derived from other species can be isolated by hybridization to the marker gene.

[0114] However, with respect to screening methods comprising an animal model to which a human gene has been introduced, not only animal homologs but also human genes may be measured as marker genes.

[0115] Thus, the influence of a candidate compound for a pharmaceutical agent on the expression level of a marker gene can be assessed by contacting an animal subject with the candidate compound and monitoring the effect of the compound on the expression level of the marker gene in a biological sample derived from the animal subject. The variation in the expression level of the marker gene in a biological sample derived from the animal subject can be monitored using the same technique as used in the testing method of the present invention described above. Furthermore, based on the evaluation, a candidate compound for a pharmaceutical agent can be selected by screening. A

compound that decreases the expression level is selected as a candidate compound for a pharmaceutical agent, when the marker gene is any one of the genes according to group (a); a compound that increases the expression level is selected as a candidate compound for a pharmaceutical agent, when the marker gene is any one of the genes according to group (b).

[0116] More specifically, a screening according to the present invention can be achieved by collecting respiratory epithelial cells as a sample from an animal subject, and comparing the expression level of a marker gene between the sample and a control with which the candidate compound has not been contacted. Methods for collecting and preparing respiratory epithelial cells are known in the art.

[0117] An animal subject may be stimulated with an allergen or IL-13 in a screening method of the present invention using an animal subj ect. The screening can be conducted by administering the candidate compound before or after the stimulation, or simultaneously, and comparing the expression level of a marker gene with that in a control. As a result, an effect of the candidate compound on the expression of a marker gene that responds to such stimulation can be evaluated. A compound having an activity to regulate the response of a marker gene to a stimulation with an allergen or IL-13 can be obtained through the screening.

[0118] These screening methods enable the selection of drugs involved in the expression of marker genes in various ways. More specifically, for example, drug candidate compounds having the following actions can be found:

[0119] When a marker gene belongs to group (a):

- suppression of a signal transduction pathway to induce the expression of the marker gene;
- suppression of the transcription activity of the marker gene; and
- inhibition of the stabilization of the transcription product of the marker gene or promotion of the decomposition thereof, etc;

[0120] When a marker gene belongs to group (b):

- activation of a signal transduction pathway to induce the expression of a marker gene;
- promotion of the transcription activity of the marker gene; and
- stabilization of the transcription product of the marker gene or inhibition of the decomposition thereof, etc;

[0121] Furthermore, methods of *in vitro* screening include, for example, a method that comprises contacting cells expressing a marker gene with a candidate compound and selecting a compound that decreases the expression level of a gene when the gene belongs to group (a), or alternatively selecting a compound that increases the expression level of a gene when the gene belongs to group (b). The screening can be conducted, for example, according to a method comprising the steps of:

(1) contacting a candidate compound with a cell expressing the marker gene;
(2) measuring the expression level of said gene; and
(3) selecting a compound that decreases the expression level of a marker gene belonging to group (a) or increases the expression level of a marker gene belonging to group (b), as compared to that in a control with which the compound has not been contacted;

[0122] In the present invention, cells expressing a marker gene can be obtained by inserting the marker gene to an appropriate expression vector, and introducing said vector into a suitable host cell. Any vector and host cell may be used as long as it is able to express a marker gene of this invention. Examples of host cells in the host-vector system are *Escherichia coli,* yeast, insect cells, animal cells, and such, and vectors that can be used for respective host cells can be appropriately selected.

[0123] Vectors may be introduced into hosts by a biological, physical, or chemical method, or such. Examples of biological methods are methods using viral vectors, methods using specific receptors, and cell-fusion methods (HVJ (Sendai virus) method, polyethylene glycol (PEG) method, electric cell fusion method, microcell-mediated chromosome transfer). Examples of physical methods are the microinjection method, electroporation method, and the method using the gene particle gun (gene gun). Examples of chemical methods are the calcium phosphate precipitation method, liposome method, DEAE-dextran method, protoplast method, erythrocyte ghost method, erythrocyte membrane ghost method, and microcapsule method.

[0124] In a screening method of the present invention, cells constituting respiratory tissues, such as epithelial cells and goblet cells can be used as cells expressing a marker gene. More specifically, epithelial cells, goblet cells, endothelial cells, smooth muscle cells, fibroblast cells, mucosal cells, and so on can be used.

[0125] Cells constituting respiratory tissues include a cell line established from the respiratory epithelium. Such a cell line can be used preferably in practicing a screening method of the present invention, because homogeneous cells

can be prepared on a large scale and the cells can be cultured by a simple method. Such a respiratory epithelial cell line can be established, for example, by the following procedure. Namely, cells are collected from the lung, trachea, or mucous membrane by protease treatment or such. In some cases, cells can be immortalized and established as cell lines through infection of a virus such as Hepatitis B virus (HBV). A previously established cell line can be used in a screening according to the present invention. Cell lines from the respiratory epithelium, which can be used in the present invention, are listed below. The corresponding accession numbers in the ATCC cell bank are shown within parentheses.

Human lung cancer cell A549 (ATCC No. CCL-185)
SHP-77 (ATCC No. CRL-2195)
Human bronchial epithelial cell BEAS-2B (ATCC No. CRL-9609)
HBE4-E6/E7 (ATCC No. CRL-2078)
NL20 (ATCC No. CRL-2503)
NCI-H727 (ATCC No. CRL-5815)
MeT-5A (ATCC No. CRL-9444)
BBM (ATCC No. CRL-9482)
BZR (ATCC No. CRL-9483)
Human mucosal endothelial cell NCI-H292 (ATCC No. CRL-1848)

[0126] A screening method of the present invention can be practiced by contacting a candidate compound with cells of a respiratory epithelial cell line described above and measuring the expression level of a marker gene within the cells. Based on the assay result, a compound that decreases the expression level of the gene is selected when the marker gene belongs to group (a) , or a compound that increases the expression level of the gene is selected when the marker gene belongs to group (b), in comparison with a control with which the candidate compound has not been contacted.

[0127] When used in a screening method of the present invention, respiratory epithelial cells can be cultured by using a method known in the art. It is preferable to use the AI method described above to culture respiratory epithelial cells. As used herein, the term the "AI method" refers to a culture method in which respiratory epithelial cells are in contact with air on the apical side and the culture medium is supplied from the basolateral membrane side. The term "air" in the AI method refers to air containing 5% CO_2 gas, which is typically used in culturing mammalian cells. In the AI method, the air is used after being sterilized with a filter.

[0128] Animal cells are typically cultured in a culture medium under a constant concentration of CO_2. However, in the AI method, respiratory epithelial cells are cultured in contact with air. The difference between the AI method and the IMM method, which is a conventional culture method for respiratory epithelial cells, is schematically illustrated in Fig. 2.

[0129] When cultured by the AI method, respiratory epithelial cells differentiate into goblet cells upon IL-13 stimulation. Thus, the possibility of selecting a compound having an effect on the process of goblet cell differentiation can be increased by pre-culturing respiratory epithelial cells using the AI method. In a screening method of the present invention, respiratory epithelial cells can be treated with IL-13. Specifically, respiratory epithelial cells may be treated with IL-13 before or after contacting a candidate compound with the respiratory epithelial cells, or simultaneously.

[0130] When cultured by the AI method, respiratory epithelial cells differentiate into goblet cells upon IL-13 stimulation. Thus, an influence of a candidate compound on the expression level of a marker gene that is expressed in the process of goblet cell differentiation can be determined by monitoring as an index, the effect of the candidate compound on respiratory epithelial cells stimulated with IL-13.

[0131] The culture method for respiratory epithelial cells according to the AI method is known in the art. For example, respiratory epithelial cells can be cultured by the AI method based on disclosures in the reports indicated below.

Yamaya M.; Kokyu Vol. 12 No. 10, pp. 1238-1243 (1993);
Yamaya et al., Am. J. Physiol. 262 (Lung Cell Mol. Physiol. 6): L713-L724 (1992)

[0132] More specifically, first, tissues of the respiratory epithelium are collected from a living body, and a suspension of respiratory epithelial cells is prepared by protease treatment. A respiratory epithelial cell line may also be used. Respiratory epithelial cells from any mammalian species including humans can be used for the screening methods of the present invention. The resulting respiratory epithelial cells are cultured on a support. A preferred cell density of respiratory epithelial cells on the support falls within about 10^4-10^8 cells/cm^2, preferably within about 10^6 cells/cm^2. Excess cells flowing out of the support are removed and the remaining is further cultured.

[0133] A material that can hold respiratory epithelial cells and supply components of the culture medium to the cells from the bottom of the cell layer, is used as a support. For example, a filter with pores whose size is too small for cells to pass through is preferably used as a support in the AI method. The filter used as a support may be coated with a material having affinity for the cells. Such materials include, for example, collagen gel. In the Examples, a commercially

available filter (Millipore; Millicell-HA) coated with Vitrogen gel (CELTRIX; Vitrogen was used after gelation) is used in the AI method. The filter is attached to the bottom of an appropriate cuvette. When a suspension of respiratory epithelial cells is added to the cuvette, a cell layer is formed on the filter. Then, the culture according to the AI method can be done by floating the collagen gel-coated cuvette in a well filled with a medium.

[0134] A typical culture medium for respiratory epithelial cells may be used in the culture according to the present invention. Specifically, such a medium includes a culture medium comprising a 1:1 mixture of Dulbecco's MEM and Ham F12, which contains 2% Ultroser G, and the following antibiotics: penicillin, streptomycin, gentamycin, and amphotericin B.

[0135] Thus, the culture according to the AI method can be practiced by adhering cells to the above-mentioned filter, continuing culture in a state in which the filter side contacts the medium and the cell side contacts air. A test compound or IL-13 can be contacted with respiratory epithelial cells by adding it to the medium. In the AI method, IL-13 is added to the medium typically at the concentration of 5-100 ng/mL, preferably of 30-80 ng/mL, for example, of 50 ng/mL in order to stimulate respiratory epithelial cells. It is preferable to use IL-13 derived from the same species from which the respiratory epithelial cells are derived.

[0136] In the screening method of this invention, expression levels of marker genes can be compared not only based on the expression levels of proteins encoded by the genes, but also based on the corresponding mRNAs detected. For performing the comparison of expression levels using mRNA, the process for preparing an mRNA sample as described above is carried out in place of the process for preparing a protein sample. Detection of mRNA and protein can be performed by known methods as described above.

[0137] Furthermore, based on the disclosure of this invention, it is possible to obtain a transcriptional regulatory region for a marker gene of this invention and construct a reporter assay system. A reporter assay system is a system for screening for a transcriptional regulatory factor that acts on a transcriptional regulatory region using as an index the expression level of a reporter gene localized downstream of the transcriptional regulatory region.

[0138] Specifically, the present invention relates to a method of screening for therapeutic agents for bronchial asthma or chronic obstructive pulmonary disease, in which a marker gene is any one selected from the group according to (a) or (b) , or a gene functionally equivalent to the marker gene, which method comprises the steps of:

(1) contacting a candidate compound with a cell into which a vector containing a transcriptional regulatory region of a marker gene and a reporter gene under the control of the transcriptional regulatory region have been introduced;
(2) measuring the activity of said reporter gene; and
(3) selecting a compound that decreases the expression level of said reporter gene when the marker gene belongs to group (a), or a compound that increases the expression level of said reporter gene when the marker gene belongs to group (b), as compared to that in a control with which the candidate compound has not been contacted;

[0139] Examples of transcription regulatory regions are promoters, enhancers, and furthermore, CAAT box and TATA box, which are normally seen in the promoter region.

[0140] Also, as reporter genes, CAT (chloramphenicol acetyltransferase) gene, luciferase gene, growth hormone genes, and such may be used.

[0141] Alternatively, a transcription regulatory region of each marker gene of this invention can be obtained as follows. That is, first, a screening is performed by a method that uses PCR or hybridization based on the nucleotide sequences of marker gene cDNA disclosed in this invention, and a genomic DNA clone containing the cDNA sequence is obtained from a human genome DNA library such as the BAC library or YAC library. Based on the obtained genomic DNA sequence, the transcription regulatory region of a cDNA disclosed in this invention is estimated, and the transcription regulatory region is obtained. A reporter construct is constructed by cloning the obtained transcription regulatory region so that it is positioned upstream of the reporter gene. The obtained reporter construct is transfected into a cultured cell strain and is made into a transformant for screening. A candidate compound is contacted with this transformant. The screening of this invention can be performed by selecting a compound capable of decreasing the expression level of a marker gene when the gene belongs to group (a) ; or selecting a compound capable of increasing the expression level of a marker gene when the marker gene belongs to group (b) .

[0142] A screening method based on the activity of a marker gene can be used as an *in vitro* screening method of the present invention. Specifically, the present invention relates to a method of screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, in which the marker gene is any one selected from the group according to (a) or (b) , or a gene functionally equivalent to the marker gene, which method comprises the steps of:

(1) contacting a candidate compound with the protein encoded by a marker gene;
(2) measuring the activity of said protein; and
(3) selecting a compound that decreases said activity when the marker gene belongs to group (a), or a compound

that increases said activity when the marker gene belongs to group (b), as compared to that in a control with which the candidate compound has not been contacted.

[0143] A compound having the activity of inhibiting the activity of a marker protein of the present invention can be selected through screening using the activity as an index, when the marker gene belongs to group (a). Such a compound that can be obtained as described above suppresses the activity of the respective marker gene belonging to group (a). Thus, the compound can control bronchial asthma or chronic obstructive pulmonary disease by inhibiting the marker protein whose expression has been induced in respiratory epithelial cells.

[0144] A compound having the activity of enhancing the activity of a marker protein can be selected through screening using the activity as an index, when the marker gene belongs to group (b). Such a compound that can be obtained as described above enhances the activity of the respective marker gene belonging to group (b). Thus, the compound can control bronchial asthma or chronic obstructive pulmonary disease by activating the marker protein whose expression has been inhibited in respiratory epithelial cells.

[0145] In addition to compound preparations synthesized by existing chemical methods, such as steroid derivatives and compound preparations synthesized by combinatorial chemistry, candidate test compounds used in such screenings include, mixtures of multiple compounds such as extracts from animal or plant tissues, or microbial cultures, and their purified preparations.

[0146] A polynucleotide, antibody, cell strain, or model animal necessary for various screening methods according to this invention can be combined in advance into a kit. A substrate compound used for the detection of a marker, a medium and vessel for cell culturing, positive and negative standard samples, and furthermore, a manual describing how to use the kit, may also be packaged in the kit. For example, such a kit may have a combination of a filter or a filter-attached cuvette to be used in the culture of respiratory epithelial cells according to the Al method, a culture well in which the cuvette is installed and the culture is maintained, a culture medium, and such.

[0147] A compound selected by a screening method of the present invention can be used as a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. An antisense nucleic acid or a ribozyme capable of suppressing the expression level of a marker gene according to (a), or a polynucleotide that suppresses the expression of the gene through an RNAi effect can also be used as a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease.

[0148] Furthermore, an antibody recognizing a peptide comprising the amino acid sequence of a protein encoded by any one of the genes according to (a) can also be used as a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. Each marker gene according to (a) is a gene whose expression level is increased in respiratory epithelial cells stimulated with IL-13. Thus, a therapeutic effect on bronchial asthma or chronic obstructive pulmonary disease can be achieved by suppressing the expression of the genes or the function of proteins encoded by the genes.

[0149] In addition, any marker gene according to (b) and the protein encoded by the gene can be used as a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease.

[0150] A therapeutic agent for an allergic disease according to this invention can be formulated by including a compound selected by a screening method of the present invention as an active ingredient, and mixing it with a physiologically acceptable carrier, excipient, diluent, or such. The therapeutic agent can be administered orally or parenterally to ameliorate the allergy symptoms.

[0151] Oral drugs can take any dosage form selected from the group of granules, powders, tablets, capsules, solutions, emulsions, suspensions, etc. Injections can include subcutaneous injections, intramuscular injections, or intraperitoneal injections.

[0152] Furthermore, when the compound to be administered comprises a protein, a therapeutic effect can be achieved by introducing a gene encoding the protein into the living body using gene therapy techniques. Techniques for treating diseases by introducing a gene encoding a therapeutically effective protein into the living body and expressing it therein are known.

[0153] Alternatively, an antisense nucleic acid, a ribozyme, or a polynucleotide that suppresses the expression of a corresponding gene by an RNAi effect can be incorporated downstream of an appropriate promoter sequence to be administered as an expression vector of an antisense RNA, a ribozyme, or an RNA having the RNAi effect. When this expression vector is introduced into mononuclear cells of an allergy patient, the therapeutic effect on the allergy can be achieved by reducing the expression level of the gene by expressing a corresponding antisense nucleic acid, ribozyme, or polynucleotide that suppresses the expression of a corresponding gene by an RNAi effect. *In vivo* or *ex vivo* methods are known for introducing the expression vector into mononuclear cells.

[0154] The expression "antisense RNA" refers to an RNA comprising a nucleotide sequence complementary to the sense sequence of a gene. When an antisense RNA is used to suppress gene expression, such an RNA typically comprises a nucleotide sequence of 15 or more consecutive nucleotides, for example, 20 or more consecutive nucleotides, or 30 or more consecutive nucleotides. For example, an antisense nucleic acid capable of hybridizing to a region

comprising an initiation codon is thought to be highly effective in suppressing the expression of the corresponding gene.

[0155] The term "ribozyme" refers to an RNA that has the catalytic activity of digesting RNA in a nucleotide sequence-specific manner. There are two types of ribozymes: hammerhead ribozymes and hairpin ribozymes. Both ribozymes are composed of a nucleotide sequence portion complementary to the region to be digested and a nucleotide sequence portion that maintains the structure required for the catalytic activity. The nucleotide sequence complementary to the region to be digested can be arbitrary. Therefore, when the nucleotide sequence of this region is set to be complementary to the nucleotide sequence of a target gene, a ribozyme can be designed to control the expression of a marker gene.

[0156] The expression "RNAi (RNA interference) effect" refers to the phenomenon where a double-stranded RNA comprising a nucleotide sequence identical to that of an mRNA strongly suppresses the expression of the mRNA. Thus, such a double-stranded RNA comprising a nucleotide sequence identical to that of the mRNA of a marker gene can be used to suppress the expression of the marker gene. A double-stranded RNA comprising a nucleotide sequence having at least 20 or more consecutive nucleotides is preferably used to exert an RNAi effect. The double strand may be composed of separate strands or a stem-and-loop structure of a single RNA chain.

[0157] With respect to an antisense nucleic acid, a ribozyme, or a polynucleotide exerting the RNAi effect, a complementary nucleotide sequence and an identical nucleotide sequence are not limited to a perfectly complementary nucleotide sequence and a perfectly identical nucleotide sequence, respectively. When having a high sequence complementarity or identity, the RNAs exhibit the activity of suppressing expression. When having typically 70% or higher, preferably 80% or higher, more preferably, 90% or higher, still more preferably 95% or higher, for example, 98% or higher identity to a nucleotide sequence or a nucleotide sequence complementary to a nucleotide sequence, an RNA can be deemed to have a high identity or complementarity.

[0158] Although the dosage may vary depending on the age, sex, body weight, and symptoms of a patient, and also treatment effects, method for administration, treatment duration, type of active ingredient contained in the drug composition, or such, it can be usually administered in the range of 0.1 mg to 500 mg, preferably 0.5 mg to 20 mg per dose for an adult. However, since the dosage varies according to various conditions, an amount less than the above-described dosage may be sufficient in some cases, whereas in others, a dosage exceeding the above-described range may be required.

[0159] The present invention also provides a DNA chip for diagnosing bronchial asthma or chronic obstructive pulmonary disease, on which a probe has been immobilized. The probe is used to detect a marker gene that is at least a single gene selected from group (a) or group (b). There is no limitation on the type of the marker gene. The more the marker gene number, the more are the markers that can be used for the diagnosis. In general, the accuracy of diagnosis is high if more markers are used. When multiple marker genes are detected, it is advantageous to select genes having different properties. Genes that are assumed to be different with respect to the mechanism of expression level variation or and the function of the encoded proteins may be defined as "genes having different properties".

[0160] Exemplary combinations of marker genes are shown below. These combinations can enhance the accuracy of allergy testing.

[Two or more genes selected from the group consisting of marker genes for proteases and protease inhibitors]

[0161] Proteases and protease inhibitors can serve as markers for the balance between tissue disruption and construction. Specifically, a chip for testing allergic bronchial asthma or chronic obstructive pulmonary disease can be prepared by accumulating probes for detecting genes selected from genes belonging to the protease group and protease inhibitor group among the marker genes of the present invention. Marker genes belonging to each group are listed at the end of this specification.

[Two or more genes selected from the group consisting of marker genes for cytokines, cytokine receptors, chemokines, chemokine receptors, CD antigens, antibodies, and antibody receptors]

[0162] Any combination of the genes listed above contains a pair of substances that are mutually related as a ligand-and-receptor. An immune response may be viewed as a result of the interaction between these substances. Accordingly, the immunological state of respiratory epithelial tissues may be determined by using these marker genes in combination. A pair of molecules in a ligand-and-receptor relationship may be selected as marker genes. Alternatively, one of the molecules in the pair may be selected as a marker gene when only that molecule has been shown to be a marker gene of the present invention.

[Two or more genes selected from the group consisting of marker genes for cytokines, extracellular matrix proteins, cytoskeletal proteins, cell adhesion molecules, and transcription factors]

[0163] Extracellular matrix proteins include collagen. Cytoskeletal proteins include keratin, small proline-rich protein

and involucrin. Cell adhesion molecules include cadherin and desmocollin. Transcription factors include jun, fos, and myc. The degree of the differentiation of respiratory epithelial tissues or remodeling (repair) of inflammatory lesions can be assessed by monitoring the expression levels of marker genes.

[Two or more genes selected from marker genes encoding enzymes]

[0164] Once a gene is selected from marker genes encoding enzymes, then it is possible to know which metabolic processes occur in respiratory epithelial cells. For example, the metabolism of lipid mediators and lipid molecules participating in the barrier function of the respiratory epithelium can be determined based on the expression levels of lipid-metabolizing enzymes. Such lipid-metabolizing enzymes include, for example, phospholipase A2, cyclooxygenase-2, prostaglandin D2 synthase, and fatty acid desaturases 1 and 2.

[0165] Alternatively, a chip for testing for bronchial asthma or chronic obstructive pulmonary disease, which contains densely immobilized probes capable of detecting genes selected from those constituting groups (a) and (b) , is effective in order to achieve a more accurate diagnosis. The selected genes are a combination of any multiple genes. Specifically, typically 10 or more, for example, 30 or more, preferably 50 or more, more preferably 60 or more, still more preferably 80 or more, or 100 or more genes can be selected from group (a). Likewise, typically 10 or more, for example, 30 or more, preferably 50 or more, more preferably 60 or more, still more preferably 80 or more, or 100 or more genes can be selected from group (b). Much more genes, for example, 150 or more, preferably 180 or more, more preferably 200 or more genes may be selected from each of the groups (a) and (b).

[0166] The present invention provides marker genes belonging to groups (a) and (b) described below for bronchial asthma or chronic obstructive pulmonary disease:

(a) group of genes whose expression levels are increased in respiratory epithelial cells upon stimulation with IL-13; and

(b) group of genes whose expression levels are decreased in respiratory epithelial cells upon stimulation with IL-13.

[0167] The use of the expression level of each gene as a marker makes it possible to establish a method of testing for bronchial asthma or chronic obstructive pulmonary disease; create animal models for bronchial asthma or chronic obstructive pulmonary disease; and screen for candidate compounds for therapeutic agents for treating the diseases. All marker genes of the present invention are genes whose expression levels vary upon stimulation with IL-13 in respiratory epithelial cells cultured by the AI method. The AI method enables the culture of respiratory epithelial cells under conditions similar to the original conditions in the body. Thus, there is a high possibility that the expression levels of marker genes found throughout the present invention are indeed altered upon stimulation with IL-13 in tissues of the respiratory tract. As described herein in Examples, the expression levels of the marker genes of the present invention are indeed increased in the mouse asthma model. Thus, all the marker genes of the present invention can be used as markers for bronchial asthma or chronic obstructive pulmonary disease, and as targets in treating bronchial asthma or chronic obstructive pulmonary disease.

[0168] The variation in the expression level of each marker gene of the present invention correlates to the disease state. Thus, bronchial asthma or chronic obstructive pulmonary disease can be treated by controlling the expression levels of the marker genes and the activities of the proteins encoded by the marker genes. For example, when the expression level of a gene of interest is increased in respiratory epithelial cells accompanied by the differentiation of the cells into goblet cells, the expression of the gene or the activity of the encoded protein is inhibited in a therapeutic strategy for treating bronchial asthma or chronic obstructive pulmonary disease. In contrast, when the expression level of a gene of interest is decreased in respiratory epithelial cells, the expression of the gene or the activity of the encoded protein is enhanced in a therapeutic strategy for treating bronchial asthma or chronic obstructive pulmonary disease. Furthermore, the marker genes can be used as novel clinical diagnostic markers to monitor bronchial asthma or chronic obstructive pulmonary disease in the treatment of the diseases.

[0169] The expression level of each marker gene provided by this invention can be easily determined, regardless of the type of allergen. Therefore, the overall pathology of an allergic reaction can be understood.

[0170] Additionally, the methods of testing for bronchial asthma or chronic obstructive pulmonary disease of this invention have low invasiveness towards patients since analysis of expression levels can be carried out using a biological sample. Furthermore, gene expression analysis has enabled highly sensitive measurements using small amounts of samples. Year after year in gene analysis technology, high throughput methods are being improved and costs are being decreased. Therefore, in the near future, the methods of testing for bronchial asthma or chronic obstructive pulmonary disease of this invention are expected to become important bedside diagnostic methods (methods that can be performed outside labs). In this sense, diagnostic value of the marker genes of this invention is high.

[0171] Furthermore, the present invention reveals that the expression level of pendrin in respiratory epithelial cells is increased upon IL-13 stimulation and that the PDS gene encoding pendrin is one of genes participating in the dif-

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ferentiation of respiratory epithelium cells into goblet cells. The expression level of pendrin is also increased in the lung of the asthma model mouse, and thus the present invention shows that the PDS gene encoding pendrin is closely associated with bronchial asthma or chronic obstructive pulmonary disease. The development of drugs for suppressing goblet cell differentiation did not start until recently. Thus, the present invention provides a new approach in drug discovery. In addition, the present Invention reveals genes participating in goblet cell differentiation, enabling a more fundamental therapy that uses the genes. Furthermore, agents that control the expression level of genes participating in goblet cell differentiation or the activity of proteins participating in goblet cell differentiation can be used in the treatment of diseases characterized by inflammation and overproduction of mucus, such as chronic obstructive pulmonary disease, cystic fibrosis, chronic sinusitis, bronchiectasis, and diffuse panbronchiolitis, as well as asthma.

[0172] Any patents, published patent applications, and any prior art references cited herein are incorporated by reference. Hereinafter, the present invention is described more specifically based on Examples, but it is not to be construed as being limited thereto.

EXAMPLE 1

The air interface (AI) method and the immersed feeding (IMM) method

1. The air interface method:

[0173] Approval for this study was obtained from the Ethical Committee of the Faculty of Medicine, The Tohoku University, Japan. Tracheal tissues derived from anatomical specimens were stretched on plates. The epithelia were removed and allowed to stand still in phosphate buffer containing protease (0.05%) at 4°C overnight. The following day, a culture medium containing fetal calf serum was added to the samples to neutralize enzyme activity, and respiratory epithelial cells were isolated by shaking the samples.

[0174] After the cell count was determined, cells were plated at the cell density of 10^6 cells/cm^2 on a filter membrane with 0.45-μm pores, being attached to the bottom of a Millicell-HA Culture Plate Insert (Millipore Corp.). At the time of plating, Vitrogen gel (Vitrogen from Celtrix Pharmaceuticals, Inc. was used after gelation) was placed on the filter membrane as a growth-supporting material, and the epithelial cells were placed thereon. The Millicell inserts were placed in a 24-well plate (Falcon) containing a culture medium, which was a 1: 1 mixture of Dulbecco's MEM and Ham F12 containing 2% Ultroser G and the antibiotics, penicillin, streptomycin, gentamycin, and amphotericin B. The cells were incubated overnight. Then, cells that had not adhered to the collagen gel were removed, and the remaining cells were cultured while the cell side was in contact with air (air interface) for approximately two weeks (See Fig. 1). The basic procedures of the AI method by which respiratory epithelial cells were cultured were the same as those described in the following reports:

Yamaya M; Kokyu, Vol. 12, No. 10, pp. 1238-1243 (1993); and
Yamaya et al., Am. J. Physiol. 262 (Lung Cell Mol. Physiol. 6): L713-L724, 1992.

2. The immersed feeding method (IMM method):

[0175] As basically done in the AI method, Vitrogen gel was placed on a filter membrane, and epithelial cells were placed thereon. The IMM method is different from the AI method in the point that the IMM method comprises adding a medium to cover the epithelial cells. Then, the filter membrane was placed in a 24-well plate (Falcon) containing the same medium as that used in the AI method. The cells were incubated for approximately two weeks (See Fig. 2). The basic procedures of the IMM method by which respiratory epithelial cells were cultured were the same as those described in the following reports:

Yamaya M; Kokyu, Vol. 12, No. 10, pp. 1238-1243 (1993); and
Yamaya et al., Am. J. Physiol. 262 (Lung Cell Mol. Physiol. 6): L713-L724, 1992.

EXAMPLE 2

Stimulation of bronchial epithelial cells with IL-13

[0176] In the AI method in Example 1, human IL-13 (Peprotech, Inc.) was added to the medium at the concentration of 50 ng/mL when changing the medium, every day for 7 days. After 7 days, human IL-13 was added to the medium when the medium was changed, every two days. After 14 days of incubation, cells were treated by PAS staining for acidic sugar chains and Alcian blue staining for basic sugar chains. The result showed that the cells had differentiated

into goblet cells comprising a huge glycoprotein, mucin.

[0177] Human IL-13 was also added in the IMM method. However, goblet cell differentiation was not observed. The objective of this study is to screen genes associated with the differentiation of respiratory epithelial cells into goblet cells upon IL-13 stimulation by the AI method. Therefore, instead of completely differentiated day-14 cells, cells that were in the process of undergoing cell differentiation were harvested at day 3 and day 7. Furthermore, cells from two different lots were used in the culture. The culture conditions used are described below.

Table 1

Lot 1			
Culture method	Stimulation with IL-13	Day 3	Day 7
AI	+	1	5
IMM	+	2	6
AI	-	3	7
IMM	-	4	8
Lot 2			
Culture method	Stimulation with IL-13	Day 3	Day 7
AI	+	9	11
AI	-	10	12

EXAMPLE 3

Preparation of RNA for GeneChips

[0178] Respiratory epithelial cells treated by the procedure described above were lysed with ISOGEN (Nippon Gene Co. , Ltd.). RNA was isolated from the solution according to the protocol attached to ISOGEN. Chloroform was added to the solution. After the mixture was stirred and centrifuged, the aqueous layer was collected. Then, isopropanol was added to the aqueous solution. After stirring and centrifuging the solution, the precipitated total RNA was collected. Approximately 5 μg to 15 μg total RNAs were extracted from sample Nos. 1 to 12. The total RNAs were analyzed for gene expression using HG-U95A to HG-U95E from Affymetrix. The type A gene chip comprises about 12,000 probes designed based on the information on the nucleotide sequences of full-length cDNAs. Each of the type B, C, D, and E gene chips comprises about 50,000 probes designed based on the information on the nucleotide sequences of ESTs.

EXAMPLE 4

Synthesis of cRNA for GeneChips

[0179] Single stranded cDNA was prepared from 5 μg of total RNA by reverse transcription using Superscript II Reverse Transcriptase (Life Technologies) following the method of Expression Analysis Technical Manual by Affymetrix, and by using T7-$(dT)_{24}$ (Amersham Pharmacia) as a primer. The T7-$(dT)_{24}$ primer comprises a nucleotide sequence in which d $(T)_{24}$ is added to a T7 promoter nucleotide sequence, as shown below.

T7-$(dT)_{24}$ primer (SEQ ID NO: 1)

5'-GGCCAGTGAATTGTAATACGACTCACTATAGGGAGGCGG-$(dT)_{24}$-3'

[0180] Next, according to Expression Analysis Technical Manual, DNA ligase, DNA polymerase I, and RNase H were added to synthesize double stranded cDNA. After phenol-chloroform extraction of cDNA, the extract was passed through Phase Lock Gels, and was purified by ethanol precipitation.

[0181] Furthermore, using BioArray High Yield RNA Transcription Labeling Kit, biotin-labeled cRNA was synthesized. Approximately 20-50 μg of biotinated cRNA was synthesized from Sample Nos. 1 to 12. Using RNeasy Spin column (QIAGEN), cRNA was purified and then fragmented by heat treatment.

[0182] 15 μg of this cRNA was added to a hybridization cocktail, according to the Expression Analysis Technical Manual. This was placed in an array and was hybridized for 16 hours at 45°C.

[0183] After the array was washed, streptavidin phycoerythrin was added for staining. After washing, a mixed anti-

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body solution of normal goat IgG and biotinylated goat IgG was added to the array. Furthermore, in order to enhance fluorescence intensity, streptavidin phycoerythrin was added again for staining. After washing, this was set in a scanner and was analyzed by the GeneChip software Suite 4.0.

EXAMPLE 5

GeneChip analysis

[0184] Data analysis was performed using the GeneChip analysis software Suite 4.0. Average Intensity (1) and Background Average (2) were determined by Absolute Analysis, and four average values were obtained (AI method, no stimulation; AI method, IL-13 stimulation; IMM method, no stimulation; and IMM method, IL-13 stimulation) by subtracting (2) from (1). These four values were used as scale factors for comparison analysis.

[0185] First, absolute analysis was performed to analyze one chip data. Positives and negatives were determined by comparing the fluorescence intensity of perfect matches and mismatches of a probe set. Determination of the three categories of Absolute Calls, i.e., P (present) , A (absent), and M (marginal), were made by values of Pos Fraction, Log Avg, and Pos/Neg:

Pos Fraction; ratio of positive pairs.
Log Avg; average of the log of fluorescence intensity ratio between probe cells of perfect match and mismatch.
Pos/Neg; ratio of the number of positive pairs and negative pairs.

[0186] Additionally, Average Difference (Avg Diff), which is the average value of the difference in fluorescence intensities between perfect matching and mismatching probe cells, was calculated for each gene.

[0187] Next, Comparison Analysis was performed on two sets of data. For example, comparison was made between the AI method, no stimulation of day 3 and the AI method, IL-13 stimulation of day 3, and the difference in expression levels was ranked as follows. Determination of the 5 categories of difference calls, which are I, D, MI, MD, and NC, were made from values of Inc/Dec, Inc Ratio, Dpos-Dneg Ratio, and Log Avg Ratio Change.
Inc: Number of probe pairs that corresponded to IL-13 stimulation and no stimulation and that were judged to have increased expression levels when stimulated by IL-13.
Dec: Number of pairs judged to have decreased expression levels when stimulated by IL-13.
Inc/Dec: Ratio of the number of pairs judged to be Inc and number of pairs judged to be Dec.
Inc Ratio: Number of pairs judged to be Inc/number of pairs actually used.
Dpos/Dneg Ratio: Ratio between the number of Neg Change subtracted from that of Pos Change, and the number of pairs actually used.
Pos Change: Difference between the number of positive pairs in Absolute Analysis of IL-13 stimulation, and the number of positive pairs in Absolute Analysis of no stimulation.
Neg Change: Difference between the number of negative pairs in Absolute Analysis of IL-13 stimulation, and the number of negative pairs in Absolute Analysis of no stimulation.
Log Avg Ratio Change: Difference between Log Avg in Absolute Analysis of IL-13 stimulation and no stimulation.
Increased: I,
Decreased: D,
Marginally Increased: MI,
Marginally Decreased: MD, and
No Change: NC

[0188] 1. A group of genes associated with goblet cell differentiation, which had been narrowed down from the genes on the gene chips of HG-U95A to HG-U95E (group (a)/ a group of genes whose expression levels were increased; and group (b)/ a group of genes whose expression levels were decreased)

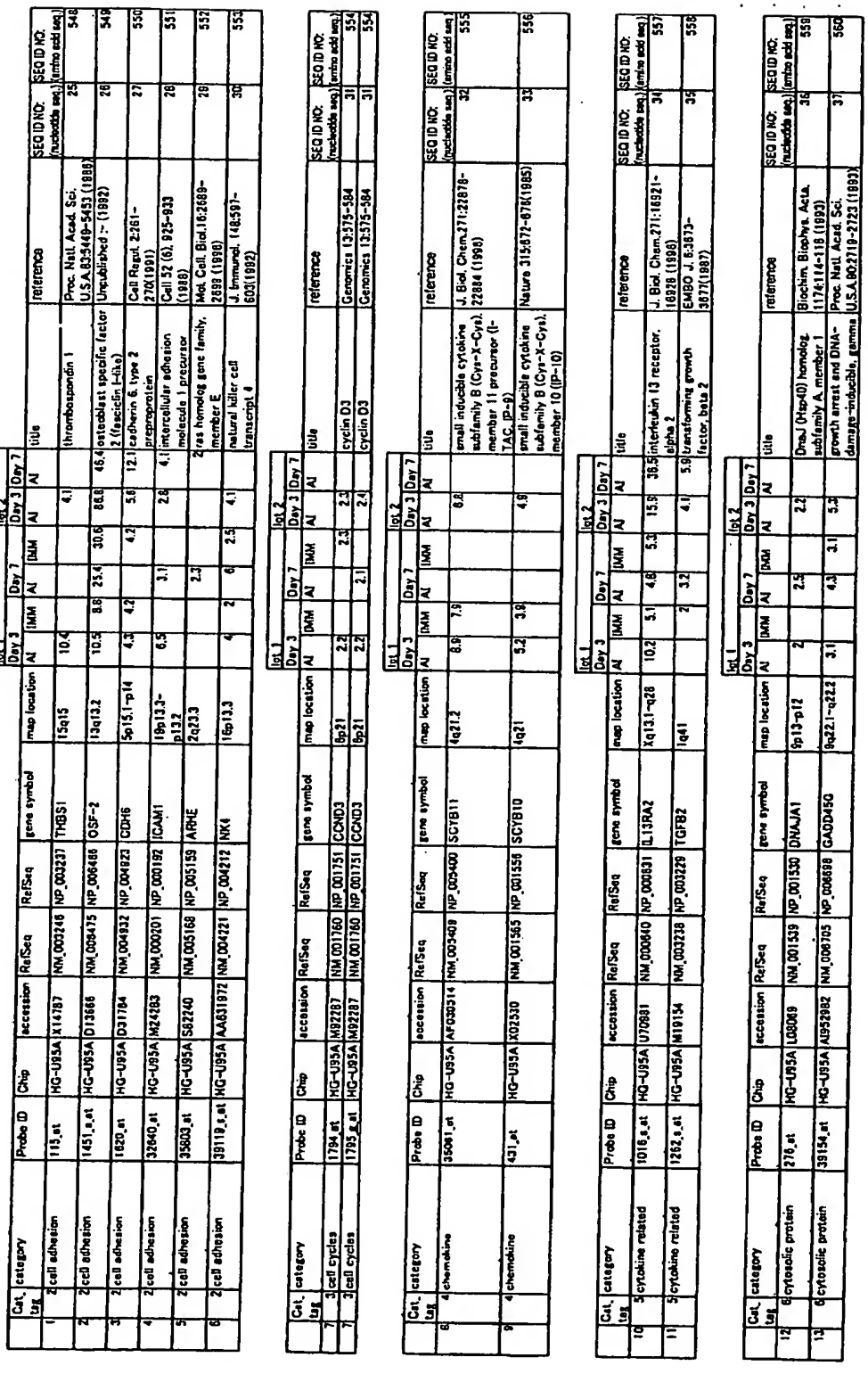
[0189] The sequences and the number of genes in gene chips A to E, whose expression levels were found to increase by two folds or more or decrease by half or less upon IL-13 stimulation in both Lots 1 and 2 under the culture conditions of the AI method, are shown in each category in Table 2. The column labeled "Increased" contains the sequences and the numbers of genes whose expression levels increased upon IL-13 stimulation. The column labeled "Decreased" contains the sequences and the numbers of genes whose expression levels decreased upon IL-13 stimulation. The annotations on the genes selected using EST chips of B to E are described according to the database NetAffx (TM) of the June/2002 version provided by Affymetrix.

Table 2

		A chip				B chip				C chip				D chip				E chip			
		increased		decreased		increased		decreased		increased		decreased		increased		decreased		increased		decreased	
	catagory	# of probe	# of gene	# of probe	# of gene	# of probe	# of gene	# of probe	# of gene	# of probe	# of gene	# of probe	# of gene	# of probe	# of gene	# of probe	# of gene	# of probe	# of gene	# of probe	# of gene
1	apoptosis	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
2	cell adhesion	6	6	6	6	2	2	2	2	0	0	0	0	0	0	1	1	1	1	1	1
3	cell cycles	2	1	0	0	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0
4	chemokine	2	2	1	1	1	1	0	0	0	0	1	1	0	0	0	0	1	1	0	0
5	cytokine related	2	2	2	2	1	1	1	1	1	1	0	0	0	0	2	2	0	0	0	0
6	cytosolic protein	2	2	2	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	enzyme	20	22	19	19	7	8	3	3	1	1	0	0	3	5	1	1	4	5	2	2
8	hypothetical protein	7	7	4	4	26	25	26	25	8	8	15	14	4	4	0	0	12	12	4	3
9	interferon-inducible protein	14	15	0	0	2	2	0	0	1	1	0	0	0	0	0	0	1	1	0	0
10	kinase	7	7	4	4	5	5	1	1	0	0	1	1	0	0	0	0	0	0	0	0
11	matrix protein	0	0	2	3	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0
12	membrane protein	11	9	12	14	3	3	1	1	3	2	1	1	0	0	0	0	2	2	0	0
13	metabolism	4	3	6	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14	MHC	4	3	2	1	1	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0
15	MMP related	4	7	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
16	oncogenesis	1	1	6	5	2	2	1	1	1	1	0	0	0	0	0	0	3	2	0	0
17	others	7	7	7	7	8	8	7	6	5	4	3	3	0	0	1	1	4	3	0	0
18	P450	0	0	3	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	phosphatase	2	2	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	protein binding protein	1	1	4	4	2	2	2	2	0	0	0	0	0	0	0	0	1	1	0	0
21	proteinase	4	4	1	1	1	1	0	0	2	2	0	0	0	0	0	0	0	0	0	0
22	proteinase inhibitor	5	4	5	4	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
23	S100	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	signal transduction	6	6	9	8	3	3	0	0	1	1	0	0	1	1	0	0	1	1	0	0
25	structural protein	2	2	9	7	1	1	1	1	2	2	1	1	0	0	0	0	0	0	0	0
26	transcription factor	9	9	6	6	2	5	1	1	0	0	2	2	0	0	0	0	0	0	0	0
27	transporter	2	2	7	7	0	0	5	5	0	0	0	0	0	0	0	0	3	3	1	1
	uncategorized	0	0	3	3	11	11	13	13	6	6	2	2	5	5	9	9	1	1	2	2
	sub total	124	124	126	122	80	83	65	63	33	31	27	28	13	15	15	15	34	33	11	10

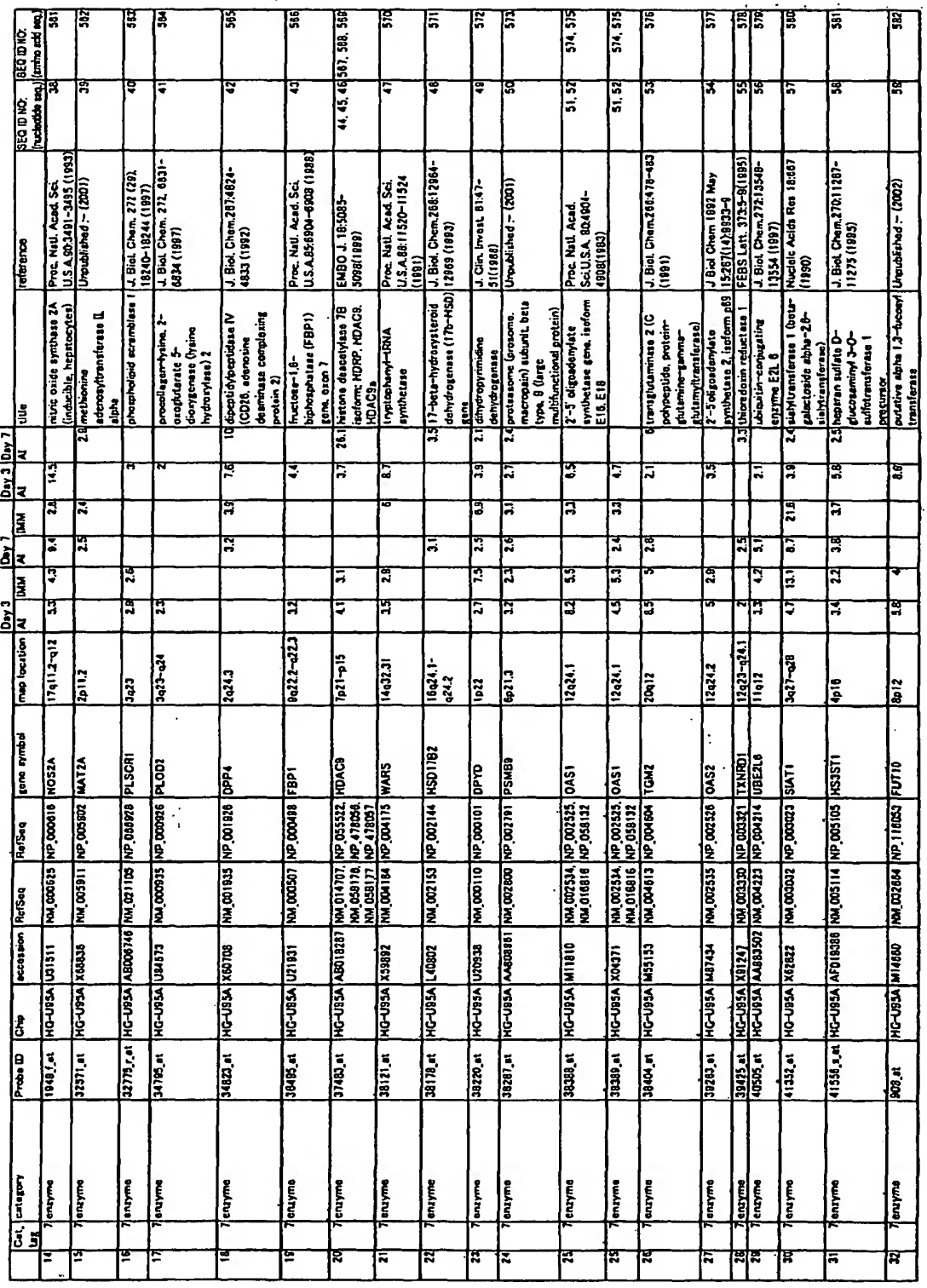
[0190] Tables 3 to 19 (a group of genes whose expression levels increased upon IL-13 stimulation) and Tables 20 to 36 (a group of genes whose expression levels decreased upon IL-13 stimulation) include lists of categorized genes on the chips of HG-U95A to HG-U95E . The Tables also include values of fold changes upon IL-13 stimulation in lot 1 and 2 when the AI method or the IMM method was used.

Table 3



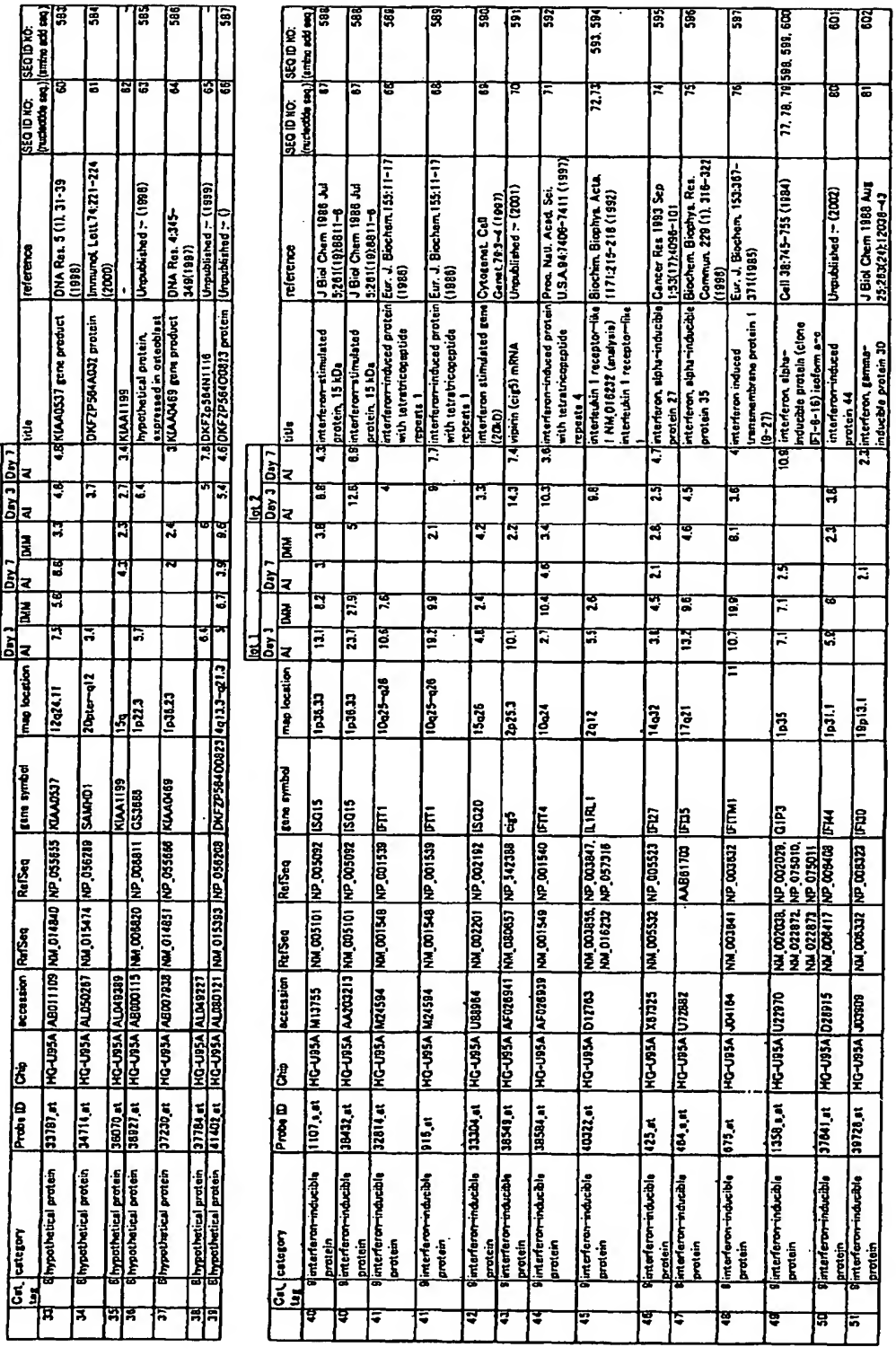
Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Igt 1 Day 3 AI	Igt 1 Day 7 IMM	Igt 1 Day 7 AI	Igt 2 Day 3 AI	Igt 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
1	2 cell adhesion	115_at	HG-U95A	X14787	NM_003246	NP_003237	THBS1	15q15	10.4		4.1			thrombospondin 1	Proc. Natl. Acad. Sci. U.S.A.83:5449-5453 (1986)	25	548
2	2 cell adhesion	1451_s_at	HG-U95A	D13666	NM_006475	NP_006466	OSF-2	13q13.2	10.5	8.8	25.4	30.6	86.8	46.4 osteoblast specific factor 2 (fasciclin I-like)	Unpublished ~ (1992)	26	549
3	2 cell adhesion	1820_at	HG-U95A	D31784	NM_004932	NP_004923	CDH6	5p15.1-p14	4.3	4.2		4.2	5.6	12.1 cadherin 6, type 2 preproprotein	Cell Regul. 2:261-270(1991)	27	550
4	2 cell adhesion	32640_at	HG-U95A	M24283	NM_000201	NP_000192	ICAM1	19p13.3-p13.2	6.5		3.1		2.8	4.1 intercellular adhesion molecule 1 precursor	Cell 52 (6), 925-933 (1988)	28	551
5	2 cell adhesion	35803_at	HG-U95A	S62140	NM_005168	NP_005159	ARHE	2q23.3			2.3			2 ras homolog gene family, member E	Mol. Cell. Biol.16:2689-2698 (1996)	29	552
6	2 cell adhesion	39118_s_at	HG-U95A	AA631972	NM_004221	NP_004212	NK4	16p13.3	4	2	6	2.5	4.1	natural killer cell transcript 4	J. Immunol. 148:597-603(1992)	30	553
7	3 cell cycles	1794_at	HG-U95A	M92287	NM_001760	NP_001751	CCND3	6p21	2.2			2.3	2.3	cyclin D3	Genomics 13:575-584	31	554
7	3 cell cycles	1795_g_at	HG-U95A	M92287	NM_001760	NP_001751	CCND3	6p21	2.2		2.1		2.4	cyclin D3	Genomics 13:575-584	31	554
8	4 chemokine	35061_at	HG-U95A	AF030314	NM_005408	NP_005400	SCYB11	4q21.2	8.8	7.9			6.8	small inducible cytokine subfamily B (Cys-X-Cys), member 11 precursor (I-TAC /IP-9)	J. Biol. Chem.271:23878-23884 (1996)	32	555
9	4 chemokine	431_at	HG-U95A	X02530	NM_001565	NP_001556	SCYB10	4q21	5.2	3.8			4.8	small inducible cytokine subfamily B (Cys-X-Cys), member 10 (IP-10)	Nature 315:672-676(1985)	33	556
10	5 cytokine related	1016_s_at	HG-U95A	U70981	NM_000640	NP_000631	IL13RA2	Xq13.1-q28	10.2	5.1	4.8	5.3	15.8	38.5 interleukin 13 receptor, alpha 2	J. Biol. Chem.271:16921-16926 (1996)	34	557
11	5 cytokine related	1262_s_at	HG-U95A	M19154	NM_003238	NP_003229	TGFB2	1q41		2	3.2		4.1	5.8 transforming growth factor, beta 2	EMBO J. 6:3673-3677(1987)	35	558
12	6 cytosolic protein	276_at	HG-U95A	L08069	NM_001539	NP_001530	DNAJA1	9p13-p12	2		2.5		2.2	DnaJ (Hsp40) homolog, subfamily A, member 1	Biochim. Biophys. Acta. 1174:114-118 (1993)	36	559
13	6 cytosolic protein	39154_at	HG-U95A	AI952982	NM_006705	NP_006698	GADD45G	9q22.1-q22.2	3.1		4.3	3.1	5.3	DnaJ (Hsp40) homolog, subfamily A, member 1 growth arrest and DNA-damage-inducible, gamma	Proc. Natl. Acad. Sci. U.S.A.90:2719-2723 (1993)	37	560

Table 4



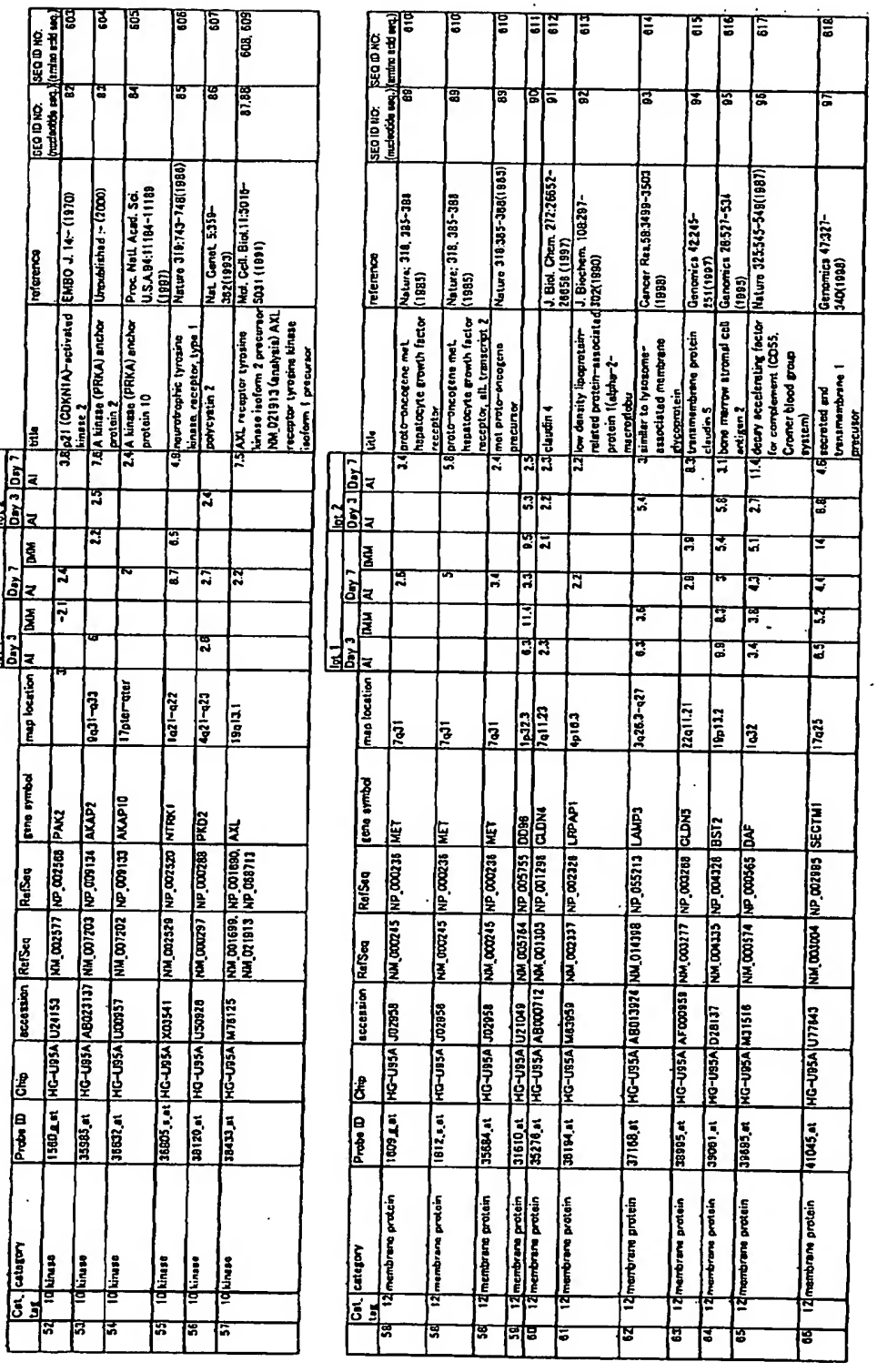
	Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Vol.1 Day 3 AI	Vol.1 Day 7 DMM	Vol.1 Day 7 AI	Vol.2 Day 3 AI	Vol.2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
14	7	enzyme	1948_f_at	HG-U95A	U31311	NM_000625	NP_000616	NOS2A	17q11.2-q12	5.5	4.3	9.4	2.8	14.5	nitric oxide synthase 2A (inducible, hepatocytes)	Proc. Natl. Acad. Sci. U.S.A.90:3491-3495 (1993)	38	581
15	7	enzyme	32371_at	HG-U95A	X68836	NM_005911	NP_005902	MAT2A	2p11.2			2.5	2.6	2.8	methionine adenosyltransferase II, alpha	Unpublished ~ (2001)	39	582
16	7	enzyme	32779_r_at	HG-U95A	ABD06746	NM_021105	NP_066928	PLSCR1	3q23	2.8	2.6			3	phospholipid scramblase 1	J. Biol. Chem. 272 (29): 18240-18244 (1997)	40	583
17	7	enzyme	34705_at	HG-U95A	U84573	NM_000935	NP_000926	PLOD1	3q23-q24	2.5				2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	J. Biol. Chem. 272, 8631-8634 (1997)	41	584
18	7	enzyme	34823_at	HG-U95A	X60708	NM_001935	NP_001926	DPP4	2q24.3		3.2	3.9	7.6	10	dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)	J. Biol. Chem.267:4624-4633 (1992)	42	585
19	7	enzyme	35405_at	HG-U95A	U21931	NM_000507	NP_000498	FBP1	9q22.2-q22.3	3.2			4.4		fructose-1,6-biphosphatase (FBP1) gene, exon 7	Proc. Natl. Acad. Sci. U.S.A.85:6904-6908 (1988)	43	586
20	7	enzyme	37483_at	HG-U95A	AB018287	NM_014707, NM_058178, NM_058177	NP_055522, NP_478056, NP_478057	HDAC9	7p21-p15	4.1	3.1		3.7	26.1	histone deacetylase 7B isoform; HDRP, HDAC8, HDAC9a	EMBO J. 18:5085-5098(1999)	44, 45, 46	587, 588, 589
21	7	enzyme	38121_at	HG-U95A	X59892	NM_004184	NP_004175	WARS	14q32.31	3.5	2.8		8	8.7	tryptophanyl-tRNA synthetase	Proc. Natl. Acad. Sci. U.S.A.86:11520-11524 (1989)	47	590
22	7	enzyme	38178_at	HG-U95A	L40802	NM_002153	NP_002144	HSD17B2	16q24.1-q24.2		3.1			3.5	17-beta-hydroxysteroid dehydrogenase (17b-HSD)	J. Biol. Chem.268:12964-12969 (1993)	48	591
23	7	enzyme	38229_at	HG-U95A	U20938	NM_000110	NP_000101	DPYD	1p22	2.7	7.5	2.3	6.9	2.1	dihydropyrimidine dehydrogenase	J. Clin. Invest. 81:47-51(1988)	49	592
24	7	enzyme	38287_at	HG-U95A	AA808861	NM_002800	NP_002791	PSMB9	6p21.3	3.2	2.3	2.6	3.1	2.4	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protein)	Unpublished ~ (2001)	50	593
25	7	enzyme	38388_at	HG-U95A	M11810	NM_002534, NM_016818	NP_002525, NP_058132	OAS1	12q24.1	8.2	5.5		3.3	6.5	2'-5' oligoadenylate synthetase gene, isoform E18, E18	Proc. Natl. Acad. Sci.U.S.A. 80:4904-4908(1983)	51, 52	594, 595
26	7	enzyme	38389_at	HG-U95A	X04371	NM_002534, NM_016816	NP_002525, NP_058132	OAS1	12q24.1	4.5	5.3	2.4	3.3	4.7			51, 52	594, 595
27	7	enzyme	38404_at	HG-U95A	M55153	NM_004613	NP_004604	TGM2	20q12	6.5	5	2.8		2.1	6 transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	J. Biol. Chem.266:478-483 (1991)	53	596
28	7	enzyme	39283_at	HG-U95A	M87434	NM_002535	NP_002326	OAS2	12q24.2	5	2.8			3.5	2'-5-oligoadenylate synthetase 2, isoform p69	J Biol Chem 1992 May 15;267(14):9933-9	54	597
29	7	enzyme	39425_at	HG-U95A	X91247	NM_003329	NP_003321	TXNRD1	12q23-q24.1	2		2.5		3.3	thioredoxin reductase 1	FEBS Lett. 373:5-9(1995)	55	598
30	7	enzyme	40505_at	HG-U95A	AA883502	NM_004223	NP_004214	UBE2L6	11q12	3.3	4.2	5.1		2.1	ubiquitin-conjugating enzyme E2L 6	J. Biol. Chem.272:13548-13554 (1997)	56	599
31	7	enzyme	41332_at	HG-U95A	X62822	NM_003032	NP_003023	SIAT1	3q27-q28	4.7	13.1	8.7	21.8	3.8	2.4 sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase)	Nucleic Acids Res 18:667 (1990)	57	600
32	7	enzyme	41536_s_at	HG-U95A	AF018388	NM_005114	NP_005105	HS3ST1	4p16	3.4	2.2	3.8	3.7	5.8	2.5 heparan sulfate D-glucosaminyl 3-O-sulfotransferase 1	J. Biol. Chem.270:11267-11275 (1995)	58	601
33	7	enzyme	908_at	HG-U95A	M14660	NM_032684	NP_116053	FUT10	8p12	1.8	4			8.6	putative alpha 1,3-fucosyltransferase	Unpublished ~ (2002)	59	602

Table 5



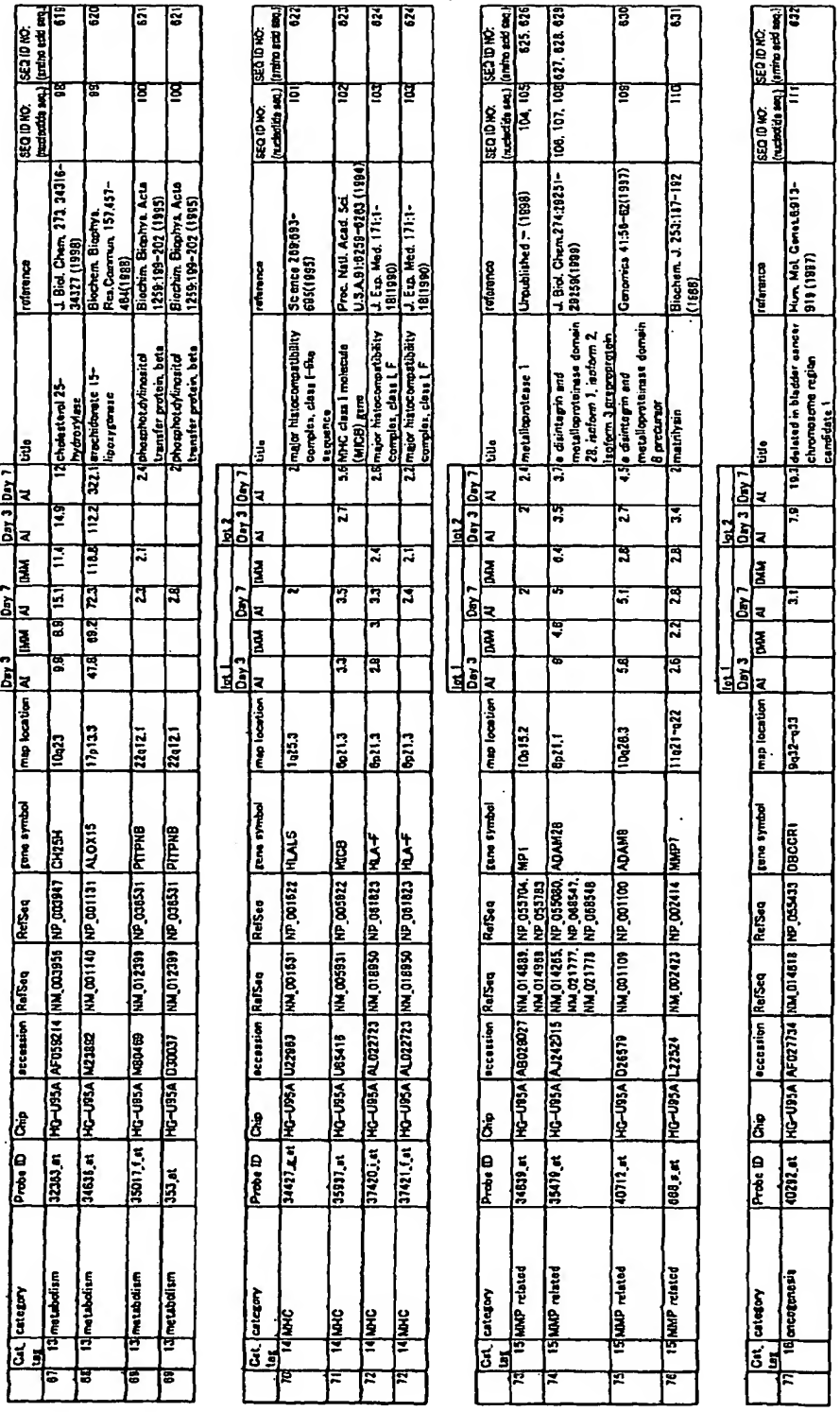
	Cat.	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lgt 1 Day 3 AI	lgt 1 Day 3 IMM	lgt 1 Day 7 AI	lgt 1 Day 7 IMM	lgt 2 Day 3 AI	lgt 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
33	8	hypothetical protein	33787_at	HG-U95A	AB011109	NM_014840	NP_055655	KIAA0537	12q24.11	7.5	5.8	8.8	3.3	4.8	4.8	KIAA0537 gene product	DNA Res. 5 (1), 31-39 (1998)	60	583
34	8	hypothetical protein	34714_at	HG-U95A	AL050287	NM_015474	NP_056289	SAMD1	20pter-q12	3.4				3.7		DKFZP564A032 protein	Immunol. Lett. 74:221-224 (2000)	61	584
35	8	hypothetical protein	36070_at	HG-U95A	AL049389			KIAA1199	15q			4.3	2.3	2.7	3.4	KIAA1199	-	62	-
36	8	hypothetical protein	36927_at	HG-U95A	AB000115	NM_006820	NP_006811	GS3688	1p22.3	3.7				6.4		hypothetical protein, expressed in osteoblast	Unpublished :- (1998)	63	585
37	8	hypothetical protein	37230_at	HG-U95A	AB007938	NM_014851	NP_055666	KIAA0469	1p36.23			2	2.4		3	KIAA0469 gene product	DNA Res. 4:345-349(1997)	64	586
38	8	hypothetical protein	37784_at	HG-U95A	AL049227					6.4				6	5	DKFZp564N1116	Unpublished :- (1999)	65	-
39	8	hypothetical protein	41402_at	HG-U95A	AL080121	NM_015393	NP_056208	DKFZP564O0823	4q13.3-q21.3	5	6.7	3.9	9.6	5.4	4.6	DKFZP564O0823 protein	Unpublished :- ()	66	587
40	9	interferon-inducible protein	1107_s_at	HG-U95A	M13755	NM_005101	NP_005092	ISG15	1p36.33	13.1	8.2	3	3.8	8.8	4.3	interferon-stimulated protein, 15 kDa	J Biol Chem 1988 Jul 5;261(19):8811-6	67	588
40	9	interferon-inducible protein	38432_at	HG-U95A	AA203213	NM_005101	NP_005092	ISG15	1p36.33	23.7	27.9		5	12.8	8.8	interferon-stimulated protein, 15 kDa	J Biol Chem 1988 Jul 5;261(19):8811-6	67	588
41	9	interferon-inducible protein	32814_at	HG-U95A	M24594	NM_001548	NP_001539	IFIT1	10q25-q26	10.6	7.6			4		interferon-induced protein with tetratricopeptide repeats 1	Eur. J. Biochem.155:11-17 (1986)	68	589
41	9	interferon-inducible protein	915_at	HG-U95A	M24594	NM_001548	NP_001539	IFIT1	10q25-q26	19.2	9.9		2.1	9	7.7	interferon-induced protein with tetratricopeptide repeats 1	Eur. J. Biochem.155:11-17 (1986)	68	589
42	9	interferon-inducible protein	33304_at	HG-U95A	U88964	NM_002201	NP_002192	ISG20	15q26	4.8	2.4		4.2	3.3		interferon stimulated gene (20kD)	Cytogenet. Cell Genet.78:3-4 (1997)	69	590
43	9	interferon-inducible protein	38548_at	HG-U95A	AF026941	NM_030657	NP_342388	cig5	2p25.3	10.1			2.2	14.3	7.4	viperin (cig5) mRNA	Unpublished :- (2001)	70	591
44	9	interferon-inducible protein	38584_at	HG-U95A	AF026939	NM_001548	NP_001540	IFIT4	10q24	2.7	10.4	4.6	3.4	10.3	3.6	interferon-induced protein with tetratricopeptide repeats 4	Proc. Natl. Acad. Sci. U.S.A.94:7406-7411 (1997)	71	592
45	9	interferon-inducible protein	40322_at	HG-U95A	D17763	NM_003855, NM_016232	NP_003847, NP_057316	IL1RL1	2q12	3.5	2.6			9.8		interleukin 1 receptor-like 1 NM_016232 (analysis) interleukin 1 receptor-like 1	Biochim. Biophys. Acta. 1171:215-218 (1992)	72,73	593, 594
46	9	interferon-inducible protein	425_at	HG-U95A	X87325	NM_005532	NP_005523	IFI27	14q32	3.1	4.5	2.1	2.8	2.5	4.7	interferon, alpha-inducible protein 27	Cancer Res 1993 Sep 1;53(17):4098-101	74	595
47	9	interferon-inducible protein	484_s_at	HG-U95A	U72882		AAB61700	IFI35	17q21	13.2	9.8		4.6	4.5		interferon, alpha-inducible protein 35	Biochem. Biophys. Res. Commun. 229 (1), 316-322 (1996)	75	596
48	9	interferon-inducible protein	879_at	HG-U95A	J04164	NM_003641	NP_003632	IFITM1		11	10.7	19.9		8.1	3.6	4	interferon induced transmembrane protein 1 (9-27)	Eur. J. Biochem. 153:387-371(1985)	76	597
49	9	interferon-inducible protein	1358_s_at	HG-U95A	U22970	NM_002038, NM_022872, NM_022873	NP_002029, NP_075010, NP_075011	G1P3	1p35	7.1	7.1	2.5			10.8	interferon, alpha-inducible protein (clone IFI-6-16) isoform a-a	Cell 38:745-755 (1984)	77, 78, 79	598, 599, 600
50	9	interferon-inducible protein	37841_at	HG-U95A	D28915	NM_006417	NP_006408	IFI44	1p31.1	5.8	6		2.3	3.6		interferon-induced protein 44	Unpublished :- (2002)	80	601
51	9	interferon-inducible protein	39728_at	HG-U95A	J03909	NM_006332	NP_006323	IFI30	19p13.1			2.1			2.3	interferon, gamma-inducible protein 30	J Biol Chem 1988 Aug 25;263(24):12038-43	81	602

Table 6



	Cat. for	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lgt 1 Day 3 AI	lgt 1 Day 3 IMM	lgt 1 Day 7 AI	lgt 1 Day 7 IMM	lgt 2 Day 3 AI	lgt 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
52	10	kinase	1560_g_at	HG-U95A	U24153	NM_002577	NP_002568	PAK2	3			-2.1	2.4		3.8	p21 (CDKN1A)-activated kinase 2	EMBO J. 14:- (1970)	82	603
53	10	kinase	35985_at	HG-U95A	AB023137	NM_007203	NP_009134	AKAP2	9q31-q33	6			2.2	2.5	7.8	A kinase (PRKA) anchor protein 2	Unpublished :- (2000)	83	604
54	10	kinase	38632_at	HG-U95A	U09057	NM_007202	NP_009133	AKAP10	17pter-qter			2			2.4	A kinase (PRKA) anchor protein 10	Proc. Natl. Acad. Sci. U.S.A.94:11184-11189 (1997)	84	605
55	10	kinase	36805_s_at	HG-U95A	X03541	NM_002320	NP_002320	NTRK1	1q21-q22			8.7	6.5		4.8	neurotrophic tyrosine kinase, receptor, type 1	Nature 316:743-748(1986)	85	606
56	10	kinase	38120_at	HG-U95A	U39928	NM_000297	NP_000288	PKD2	4q21-q23	2.8	2.7		2.4			polycystin 2	Nat. Genet. 5:319-323(1993)	86	607
57	10	kinase	38433_at	HG-U95A	M76125	NM_001699, NM_021913	NP_001690, NP_068713	AXL	19q13.1			2.2			7.5	AXL receptor tyrosine kinase isoform 2 precursor, NM_021913 (analysis) AXL receptor tyrosine kinase isoform 1 precursor	Mol. Cell. Biol.11:3010-5031 (1991)	87,88	608, 609
58	12	membrane protein	1809_g_at	HG-U95A	J02958	NM_000245	NP_000235	MET	7q31			2.6			3.4	proto-oncogene met, hepatocyte growth factor receptor	Nature; 318, 385-388 (1985)	89	610
58	12	membrane protein	1812_s_at	HG-U95A	J02958	NM_000245	NP_000236	MET	7q31			5			5.8	proto-oncogene met, hepatocyte growth factor receptor, alt. transcript 2	Nature; 318, 385-388 (1985)	89	610
58	12	membrane protein	35684_at	HG-U95A	J02958	NM_000245	NP_000236	MET	7q31			3.4			2.4	met proto-oncogene precursor	Nature 318:385-388(1985)	89	610
59	12	membrane protein	31610_at	HG-U95A	U21049	NM_005755	NP_005755	DD96	1p32.3	6.3	11.4	3.3	9.5	5.3	2.5			90	611
60	12	membrane protein	35270_at	HG-U95A	AB000712	NM_001303	NP_001294	CLDN4	7q11.23	2.3			2.1	2.2	2.3	claudin 4	J. Biol. Chem. 272:26652-26658 (1997)	91	612
61	12	membrane protein	38194_at	HG-U95A	M63959	NM_002357	NP_002328	LRPAP1	4p16.3			2.2			2.2	low density lipoprotein-related protein-associated protein 1(alpha-2-macroglobu	J. Biochem. 108:297-302(1990)	92	613
62	12	membrane protein	37168_at	HG-U95A	AB013924	NM_014398	NP_055213	LAMP3	3q26.3-q27	6.3	3.6			5.4	3	similar to lysosome-associated membrane glycoprotein	Cancer Res.58:3499-3503 (1998)	93	614
63	12	membrane protein	38895_at	HG-U95A	AF000959	NM_003277	NP_003268	CLDN3	22q11.21			2.8	3.9		8.3	transmembrane protein claudin 5	Genomics 42:245-251(1997)	94	615
64	12	membrane protein	39061_at	HG-U95A	D28137	NM_004335	NP_004326	BST2	19p13.2	6.8	8.2	3	5.4	5.8	3.1	bone marrow stromal cell antigen 2	Genomics 28:527-534 (1995)	95	616
65	12	membrane protein	33685_at	HG-U95A	M31516	NM_000574	NP_000565	DAF	1q32	3.4	3.8	4.3	5.1	2.7	11.4	decay accelerating factor for complement (CD55, Cromer blood group system)	Nature 323:545-548(1987)	96	617
66	12	membrane protein	41045_at	HG-U95A	U77643	NM_003004	NP_002995	SECTM1	17q25	6.5	5.2	4.1	14	6.8	4.6	secreted and transmembrane 1 precursor	Genomics 47:327-340(1998)	97	618

Table 7



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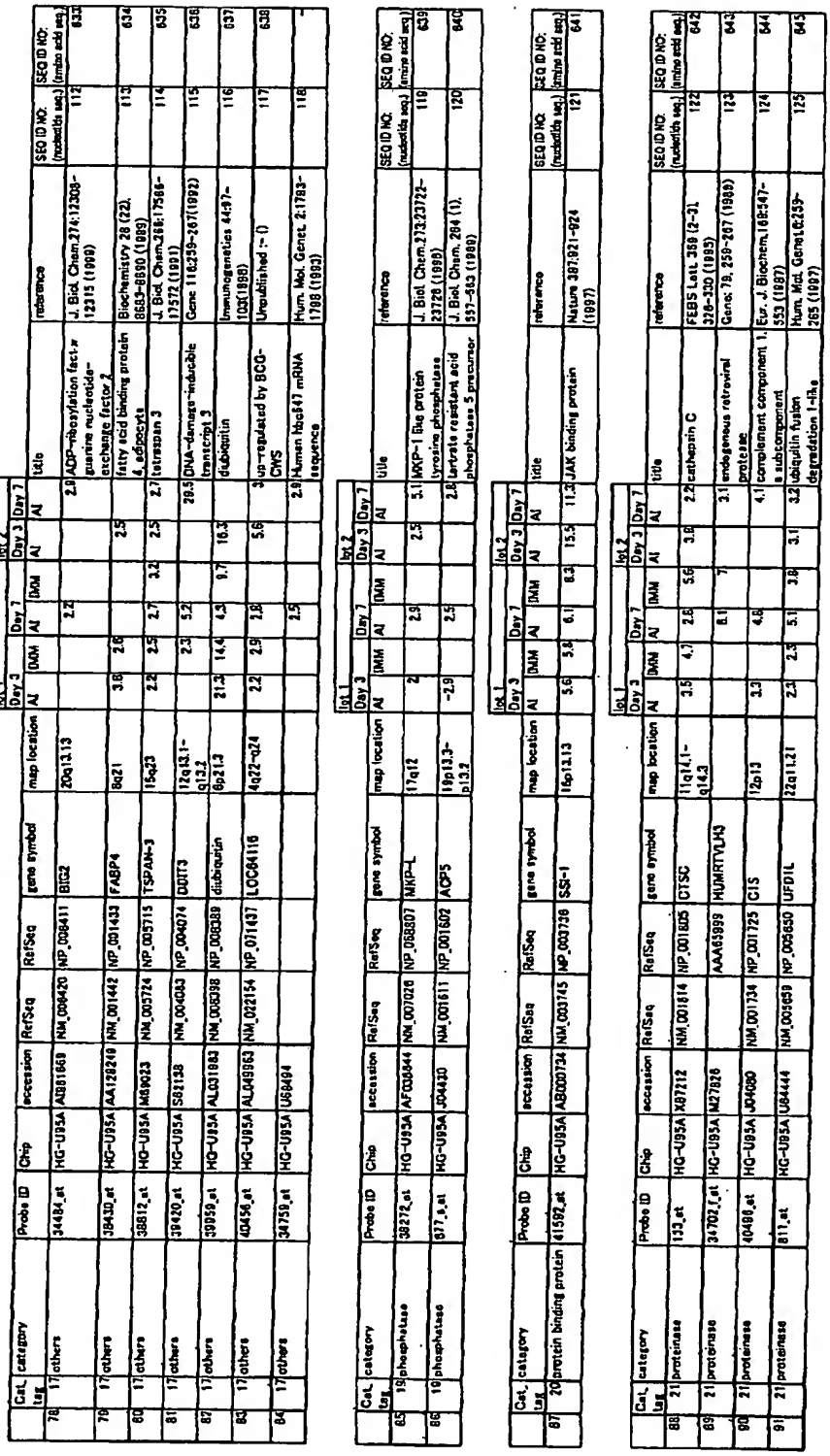
67	13	metabolism	32383_at	HG-U95A	AF059214	NM_003947	CH25H	10q23	9.8	8.8	15.1	11.4	14.9	12	cholesterol 25-hydroxylase	J. Biol. Chem. 273, 34316-34327 (1998)	98	619
68	13	metabolism	34631_at	HG-U95A	M23892	NM_001140	ALOX15	17p13.3	47.8	69.2	72.5	118.8	112.2	322.1	arachidonate 15-lipoxygenase	Biochem. Biophys. Res.Commun. 157,457-464(1988)	99	620
69	13	metabolism	35017_f_at	HG-U95A	M80469	NM_012399	PITPNB	22q12.1			2.3	2.1		2.4	phosphatidylinositol transfer protein, beta	Biochim. Biophys. Acta 1259:199-202 (1995)	100	621
69	13	metabolism	353_at	HG-U95A	D30037	NM_012399	PITPNB	22q12.1			2.8			2	phosphatidylinositol transfer protein, beta	Biochim. Biophys. Acta 1259:199-202 (1995)	100	621

	Cat.	category	Probe ID	Chip	accession	RefSeq	gene symbol	map location	Lot 1 Day 3 AI	Lot 1 Day 3 IMM	Lot 1 Day 7 AI	Lot 1 Day 7 IMM	Lot 2 Day 3 AI	Lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
70	14	MHC	34427_at	HG-U95A	U22963	NM_001631	HLALS	1q35.3			2			2	major histocompatibility complex, class I-like sequence	Science 269:693-695(1995)	101	622
71	14	MHC	35937_at	HG-U95A	U65415	NM_005931	MICB	6p21.3	3.3		3.5		2.7	3.5	MHC class I molecule (MICB) gene	Proc. Natl. Acad. Sci. U.S.A.91:8259-8263 (1994)	102	623
72	14	MHC	37420_i_at	HG-U95A	AL022723	NM_018950	HLA-F	6p21.3	2.8	3	3.3	2.4		2.8	major histocompatibility complex, class I F	J. Exp. Med. 171:1-18(1990)	103	624
72	14	MHC	37421_f_at	HG-U95A	AL022723	NM_018950	HLA-F	6p21.3			2.4	2.1		2.2	major histocompatibility complex, class I F	J. Exp. Med. 171:1-18(1990)	103	624

	Cat.	category	Probe ID	Chip	accession	RefSeq	gene symbol	map location	Lot 1 Day 3 AI	Lot 1 Day 3 IMM	Lot 1 Day 7 AI	Lot 1 Day 7 IMM	Lot 2 Day 3 AI	Lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
73	15	MMP related	34639_at	HG-U95A	AB023027	NM_014889, NM_014988	MP1	10q15.2			2		2	2.4	metalloprotease 1	Unpublished – (1998)	104, 105	625, 626
74	15	MMP related	35419_at	HG-U95A	AJ242215	NM_014265, NM_021777, NM_021778	ADAM28	6p21.1	6	4.8	5	6.4	3.5	3.7	a disintegrin and metalloproteinase domain 28, isoform 1, isoform 2, isoform 3 precursor	J. Biol. Chem.274:28231-28236(1999)	106, 107, 108	627, 628, 629
75	15	MMP related	40712_at	HG-U95A	D26579	NM_001109	ADAM8	10q26.3	5.8		5.1	2.8	2.7	4.3	a disintegrin and metalloproteinase domain 8 precursor	Genomics 41:56-62(1997)	109	630
76	15	MMP related	668_s_at	HG-U95A	L12524	NM_002423	MMP7	11q21-q22	2.6	2.2	2.8	2.8	3.4	2	matrilysin	Biochem. J. 253:187-192 (1988)	110	631

	Cat.	category	Probe ID	Chip	accession	RefSeq	gene symbol	map location	Lot 1 Day 3 AI	Lot 1 Day 3 IMM	Lot 1 Day 7 AI	Lot 1 Day 7 IMM	Lot 2 Day 3 AI	Lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
77	16	oncogenesis	40282_at	HG-U95A	AF027734	NM_014818	DBCCR1	9q32-q33			3.1		7.9	19.3	deleted in bladder cancer chromosome region candidate 1	Hum. Mol. Genet.6:913-919 (1997)	111	632

Table 8



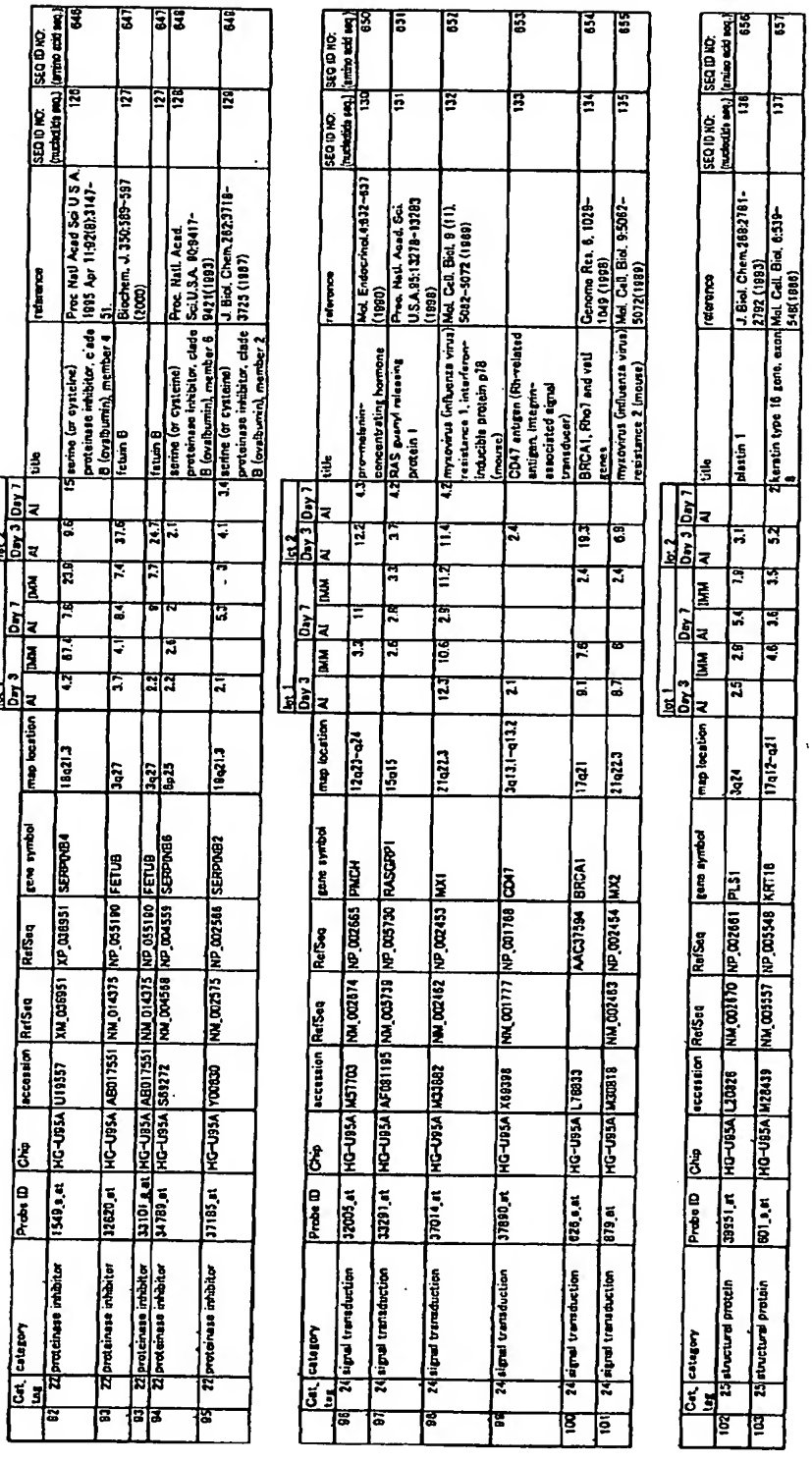
	Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 3 DMM	lot 1 Day 7 AI	lot 1 Day 7 DMM	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
78	17	others	34484_at	HG-U95A	AB81868	NM_006420	NP_006411	BIG2	20q13.13			2.2			2.9	ADP-ribosylation factor guanine nucleotide-exchange factor 2	J. Biol. Chem.274:12308-12315 (1999)	112	633
79	17	others	38430_at	HG-U95A	AA128240	NM_001442	NP_001433	FABP4	8q21	3.6	2.6			2.5		fatty acid binding protein 4, adipocyte	Biochemistry 28 (22): 8683-8690 (1989)	113	634
80	17	others	38812_at	HG-U95A	M69023	NM_005724	NP_005715	TSPAN-3	15q23	2.2	2.5	2.7	3.2	2.5	2.7	tetraspan 3	J. Biol. Chem.266:17566-17572 (1991)	114	635
81	17	others	39420_at	HG-U95A	S82138	NM_004083	NP_004074	DDIT3	12q13.1-q13.2		2.3	5.2			29.5	DNA-damage-inducible transcript 3	Gene 116:259-267(1992)	115	636
82	17	others	39959_at	HG-U95A	AL031983	NM_006389	NP_006380	dubinarin	6p21.3	21.3	14.4	4.5	9.7	16.3		dubinarin	Immunogenetics 44:97-100(1996)	116	637
83	17	others	40456_at	HG-U95A	AL049963	NM_022154	NP_071437	LOC84116	4q22-q24	2.2	2.9	1.8		5.6	3	up-regulated by BCG-CWS	Unpublished :- (1)	117	638
84	17	others	34759_at	HG-U95A	U68494							2.5			2.9	Human hbc647 mRNA sequence	Hum. Mol. Genet. 2:1783-1788 (1993)	118	-

	Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 3 DMM	lot 1 Day 7 AI	lot 1 Day 7 DMM	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
85	19	phosphatase	38272_at	HG-U95A	AF030844	NM_007026	NP_058807	MKP-L	17q12		2		2.9		2.5	MKP-1 like protein tyrosine phosphatase	J. Biol. Chem.273:23722-23728 (1998)	119	639
86	19	phosphatase	877_s_at	HG-U95A	J04430	NM_001611	NP_001602	ACP5	19p13.3-p13.2	-2.9		2.5			2.8	tartrate resistant acid phosphatase 5 precursor	J. Biol. Chem. 264 (1): 557-563 (1989)	120	640

	Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 3 DMM	lot 1 Day 7 AI	lot 1 Day 7 DMM	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
87	20	protein binding protein	41592_at	HG-U95A	AB000734	NM_003745	NP_000736	SSI-1	16p12.13	5.6	3.8	6.1	8.3	15.5	11.2	JAK binding protein	Nature 387:921-924 (1997)	121	641

	Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 3 DMM	lot 1 Day 7 AI	lot 1 Day 7 DMM	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
88	21	proteinase	153_at	HG-U95A	X87212	NM_001814	NP_001805	CTSC	11q14.1-q14.3	3.5	4.7	2.8	5.6	3.8	2.2	cathepsin C	FEBS Lett. 350 (2-3): 326-330 (1993)	122	642
89	21	proteinase	34702_f_at	HG-U95A	M27826		AAA63999	HUMRTVLH3					8.1	7	3.1	endogenous retroviral protease	Gene; 79, 259-267 (1989)	123	643
90	21	proteinase	40486_at	HG-U95A	J04080	NM_001734	NP_001725	C1S	12p13	3.3		4.8			4.1	complement component 1, s subcomponent	Eur. J. Biochem.168:547-553 (1987)	124	644
91	21	proteinase	811_at	HG-U95A	U84444	NM_003650	NP_003650	UFDIL	22q11.21	2.5	2.5	5.1	3.8	3.1	3.2	ubiquitin fusion degradation 1-like	Hum. Mol. Genet.6:259-265 (1997)	125	645

Table 9



Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Jet 1 Day 3 AI	Jet 1 Day 7 IMM	Jet 1 Day 7 AI	Jet 2 Day 3 AI	Jet 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
92	22	proteinase inhibitor	1549_s_at	HG-U95A	U19557	XM_008951	XP_008951	SERPINB4	18q21.3	4.2	81.4	7.8	23.9	9.8	15 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4	Proc Natl Acad Sci U S A 1995 Apr 11;92(8):3147-51	126	646
93	22	proteinase inhibitor	32620_at	HG-U95A	AB017551	NM_014375	NP_055190	FETUB	3q27	3.7	4.1	8.4	7.4	31.6	fetuin B	Biochem. J. 350:589-597 (2000)	127	647
93	22	proteinase inhibitor	33101_s_at	HG-U95A	AB017551	NM_014375	NP_055190	FETUB	3q27	2.2	9	7.7	24.7		fetuin B		127	647
94	22	proteinase inhibitor	34789_at	HG-U95A	S69272	NM_004568	NP_004559	SERPINB6	6p25	2.2	2		2.1		serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6	Proc. Natl. Acad. Sci. U.S.A. 90:8417-8421(1993)	128	648
95	22	proteinase inhibitor	37185_at	HG-U95A	Y00630	NM_002975	NP_002966	SERPINB2	18q21.3	2.1		5.3	- 3	4.1	3.4 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	J. Biol. Chem.262:3716-3725 (1987)	129	648

Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Jet 1 Day 3 AI	Jet 1 Day 7 IMM	Jet 1 Day 7 AI	Jet 2 Day 3 AI	Jet 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
96	24	signal transduction	32005_at	HG-U95A	M57703	NM_002874	NP_002865	PNCH	12q23-q24		3.2	11	12.2	4.3	pro-melanin-concentrating hormone	Mol. Endocrinol.4:932-937 (1990)	130	650
97	24	signal transduction	33291_at	HG-U95A	AF081185	NM_003730	NP_003730	RASGRP1	15q15		2.6	2.8	3.3	3.7	4.2 RAS guanyl releasing protein 1	Proc. Natl. Acad. Sci. U.S.A.95:13278-13283 (1998)	131	651
98	24	signal transduction	37014_at	HG-U95A	M31932	NM_002462	NP_002453	MX1	21q22.3	12.3	10.6	2.9	11.2	11.4	4.2 myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	Mol. Cell. Biol. 9 (11): 5062-5072 (1989)	132	652
99	24	signal transduction	37890_at	HG-U95A	X68398	NM_001777	NP_001768	CD47	3q13.1-q13.2	2.1			2.4		CD47 antigen (Rh-related antigen, integrin-associated signal transducer)		133	653
100	24	signal transduction	828_s_at	HG-U95A	L78833		AAC37594	BRCA1	17q21	9.1	7.6		2.4	19.3	BRCA1, Rho1 and vav1 genes	Genome Res. 6, 1028-1049 (1996)	134	654
101	24	signal transduction	879_at	HG-U95A	M30818	NM_002463	NP_002454	MX2	21q22.3	8.7	8		2.4	6.8	myxovirus (influenza virus) resistance 2 (mouse)	Mol. Cell. Biol. 9:5062-5072(1989)	135	655

Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Jet 1 Day 3 AI	Jet 1 Day 7 IMM	Jet 1 Day 7 AI	Jet 2 Day 3 AI	Jet 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
102	25	structural protein	39951_at	HG-U95A	L20826	NM_001170	NP_002661	PLS1	3q24	2.5	2.9	5.4	1.8	3.1	plastin 1	J. Biol. Chem.268:27781-27792 (1993)	136	656
103	25	structural protein	901_s_at	HG-U95A	M28439	NM_005557	NP_005548	KRT18	17q12-q21	4.6	3.6	3.5	5.2	2	keratin type 18 gene, exon 8	Mol. Cell. Biol. 6:519-545(1986)	137	657

Table 10

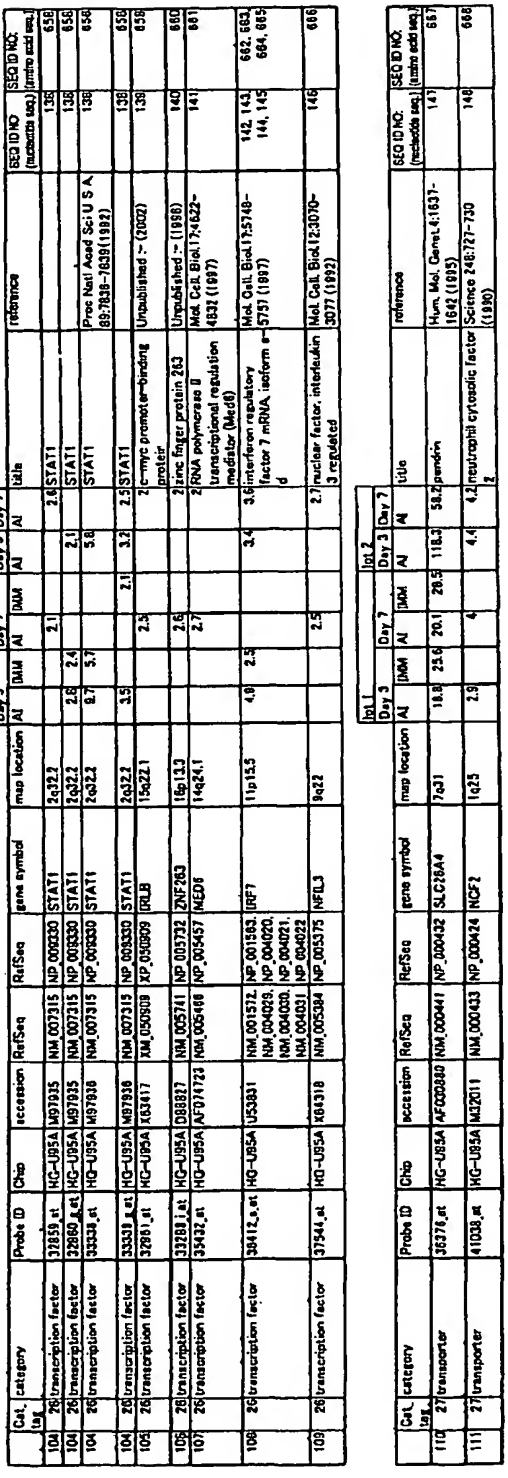
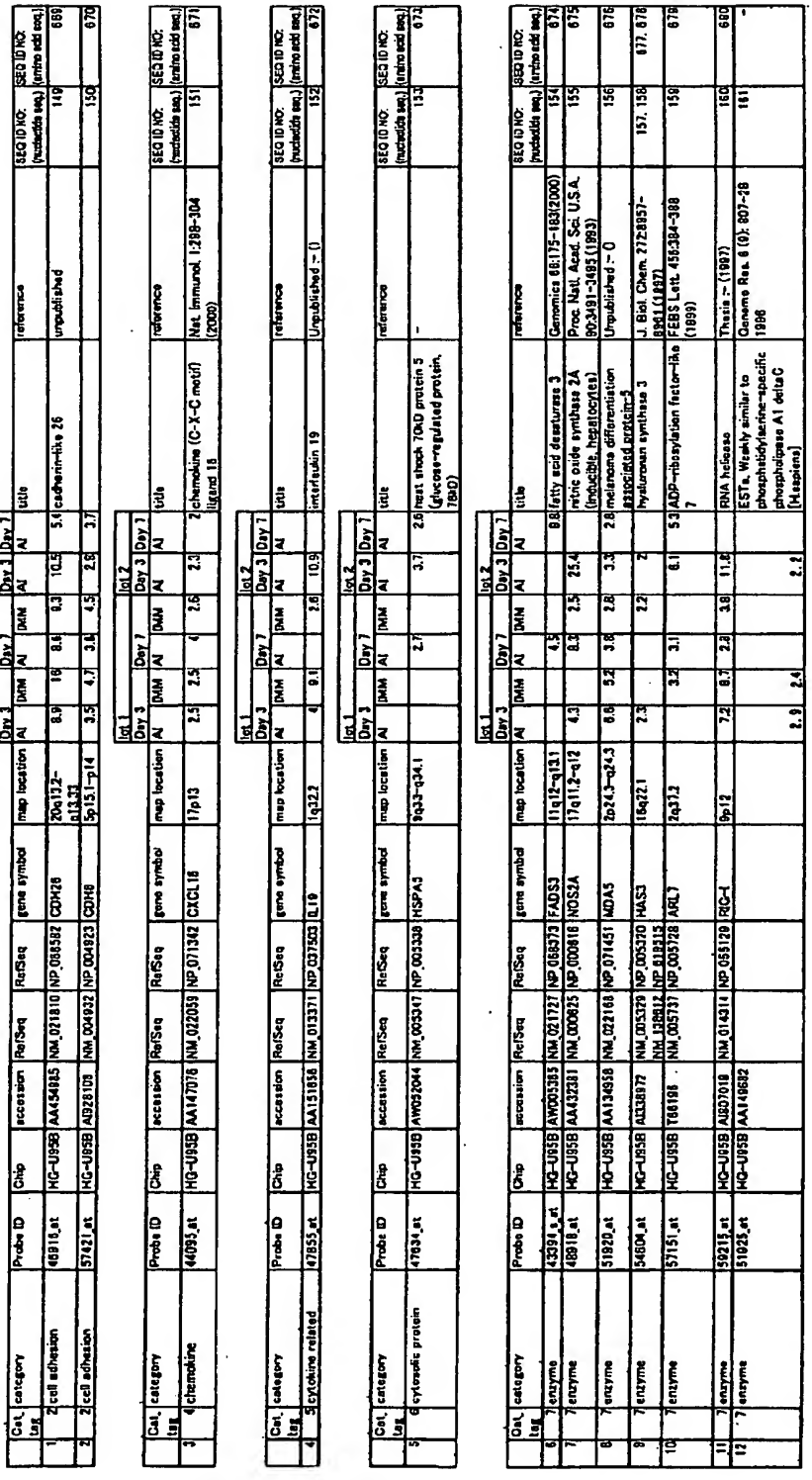


Table 11



Cat_tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 7 DMN	lot 1 Day 7 AI	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
1	2 cell adhesion	46918_at	HG-U95B	AA454885	NM_021810	NP_068582	CDH26	20q13.2-q13.33	8.9	16	8.6	6.3	10.5	5.4 cadherin-like 26	unpublished	149	669
2	2 cell adhesion	57421_at	HG-U95B	AI928109	NM_004932	NP_004923	CDH8	5p15.1-p14	3.5	4.7	3.8	4.5	2.8	3.7		150	670

Cat_tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 7 DMN	lot 1 Day 7 AI	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
3	4 chemokine	44091_at	HG-U95B	AA147078	NM_022059	NP_071342	CXCL16	17p13	2.5	2.5	4	2.6	2.3	2 chemokine (C-X-C motif) ligand 16	Nat. Immunol. 1:398-304 (2000)	151	671

Cat_tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 7 DMN	lot 1 Day 7 AI	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
4	5 cytokine related	47855_at	HG-U95B	AA151858	NM_013371	NP_037503	IL19	1q32.2	4	9.1	2.6	10.9		interleukin 19	Unpublished :- ()	152	672

Cat_tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 7 DMN	lot 1 Day 7 AI	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
5	6 cytosolic protein	47634_at	HG-U95B	AW092044	NM_005347	NP_005338	HSPA5	9q33-q34.1		2.7		3.7	2.6	heat shock 70kD protein 5 (glucose-regulated protein, 78kD)	-	153	673

Cat_tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 7 DMN	lot 1 Day 7 AI	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
6	7 enzyme	43394_s_at	HG-U95B	AW005385	NM_021727	NP_068373	FADS3	11q12-q13.1		4.5			0.8	fatty acid desaturase 3	Genomics 66:175-183(2000)	154	674
7	7 enzyme	46918_at	HG-U95B	AA432381	NM_000625	NP_000616	NOS2A	17q11.2-q12	4.3	8.3	2.5	25.4		nitric oxide synthase 2A (inducible, hepatocytes)	Proc. Natl. Acad. Sci. U.S.A. 90:3491-3495(1993)	155	675
8	7 enzyme	51920_at	HG-U95B	AA134958	NM_022168	NP_071451	MDA5	2q24.3-q24.3	8.6	5.2	3.8	2.8	3.3	2.8 melanoma differentiation associated protein-5	Unpublished :- 0	156	676
9	7 enzyme	54604_at	HG-U95B	AI338972	NM_005329	NP_005370	HAS3	16q22.1	2.3		2.2	2		hyaluronan synthase 3	J. Biol. Chem. 272:8957-8961(1997)	157, 158	677, 678
10	7 enzyme	57151_at	HG-U95B	T66198	NM_138812 NM_005737	NP_619315 NP_005728	ARL7	2q31.2	3.2	3.1		6.1	5.3	ADP-ribosylation factor-like 7	FEBS Lett. 458:384-388 (1999)	159	678
11	7 enzyme	59215_at	HG-U95B	AI807018	NM_014314	NP_055129	RIC-1	9p12	7.2	8.7	2.8	3.8	11.8	RIN3 helicase	Thesis :- (1997)	160	680
12	7 enzyme	51925_at	HG-U95B	AA148682				9p12	2.9	2.4			2.2	EST, Weakly similar to phosphatidylserine-specific phospholipase A1 delta C [Homo sapiens]	Genome Res. 6 (9): 807-28 1996	161	-

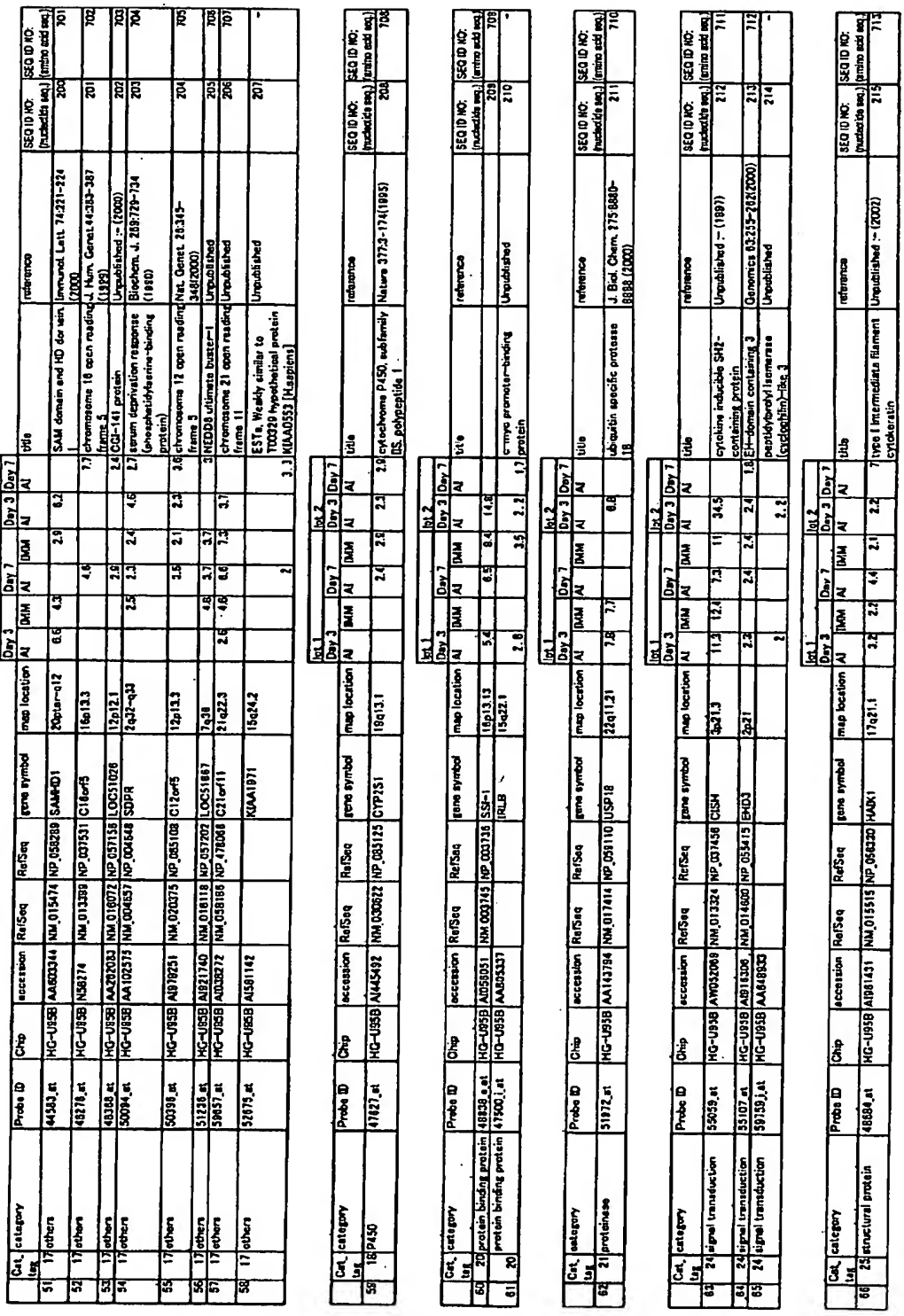
Table 12

	Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Tgt.1 Day 3 AI	Tgt.1 Day 7 DMN	Tgt.1 Day 7 AI	Tgt.2 Day 3 AI	Tgt.2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
13	8	hypothetical protein	43366_at	HG-U95B	AI976079	NM_018043	NP_060513	FLJ10261	11q13.1	7.8	8.2	10.6	8.4	11.2	7.9	hypothetical protein FLJ10261	Unpublished (2000)	162	681
15	8	hypothetical protein	43163_at	HG-U95B	AI700434	NM_018043	NP_060513	FLJ10261	11q13.1	6.6	8.7		14.4		8.2	hypothetical protein FLJ10261	Unpublished (2000)	162	681
14	8	hypothetical protein	48233_at	HG-U95B	AI341483	NM_017812	NP_060282	FLJ20420	7q32.3		2.1				-	hypothetical protein FLJ20420	Unpublished	163	682
15	8	hypothetical protein	50109_at	HG-U95B	AI830208	NM_024920	NP_078196	FLJ14281	4q22.3		2.5				2	hypothetical protein FLJ14281	Unpublished	164	683
16	8	hypothetical protein	53177_at	HG-U95B	AI872353	NM_022750	NP_073587	FLJ22693	7q34	2.8	2.1		2.2	2.2	1.6	hypothetical protein FLJ22693	Genome Res. 11:422-435(2001)	165	684
17	8	hypothetical protein	56858_at	HG-U95B	AI378849	NM_024724	NP_078000	FLJ22332	3q23		3.4				3.0	hypothetical protein FLJ22332	Unpublished (2001)	166	685
18	8	hypothetical protein	57197_at	HG-U95B	AA806378	NM_030915	NP_112177	DKFZP586J091	2p23.3	8.4	8.2	11.3	4.2	45.3	15.2	hypothetical protein DKFZp586J091	Genome Res. 11:422-435 (2001)	167	686
19	8	hypothetical protein	58857_at	HG-U95B	AI620475	NM_017912	NP_060382	C21orf11	21q22.3	8.8	6.2	2.1	6	7.1	2.4	hypothetical protein FLJ20637	Unpublished	168	687
20	8	hypothetical protein	44127_at	HG-U95B	AA804375							2.5		2.1	1.9	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 994846	Unpublished	169	-
21	8	hypothetical protein	48858_at	HG-U95B	AI700705										1.5	FLJ31051 fis, clone HSYRA2000803, weakly similar to MYOSIN HEAVY CHAIN, CLONE 293	Unpublished	170	-
22	0	hypothetical protein	47087_at	HG-U95B	AI310524					3.6			2		1.5	Homo sapiens cDNA	Unpublished	171	-
23	0	hypothetical protein	48826_s_at	HG-U95B	AW019985										14.7	Homo sapiens mRNA; cDNA DKFZp434D0818 (from clone DKFZp434D0818)	Genomics 23: 42-50 1994	172	-
24	0	hypothetical protein	52307_at	HG-U95B	AA382326					2.4	3.8	3.7	1.2	3.7	3.7	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 994846	Unpublished	173	-
25	0	hypothetical protein	52327_s_at	HG-U95B	AI869346					2.3	2.3	2.7	2.1	1.2	2.5	Homo sapiens mRNA; cDNA DKFZp434G227 (from clone DKFZp434G227)	Unpublished	174	-
26	0	hypothetical protein	52539_at	HG-U95B	AA430478					3.8		4.1		2.2	10.1	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 994846	Unpublished	175	-
27	0	hypothetical protein	52422_at	HG-U95B	AA541787					2.3	2.6			2.2	3.9	Homo sapiens cDNA FLJ11812 fis, clone HEMBA1008394	Unpublished	176	-
28	0	hypothetical protein	53010_at	HG-U95B	AI809925					3.1		3.6	2.8	2.2		Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2088071	Unpublished	177	-
29	0	hypothetical protein	53061_at	HG-U95B	AI718385					4.6			3.2	2.2		Homo sapiens cDNA: FLJ21425 fis, clone COL04182	Unpublished	178	-
30	0	hypothetical protein	54033_at	HG-U95B	AI859827					4.2	8.3	4.2	11	4.6	3	FLJ23547 fis, clone HSI00356	Unpublished	179	-
31	0	hypothetical protein	54886_at	HG-U95B	AI565105					2.8	2.2	2.4		2.2	2.4	Homo sapiens mRNA; cDNA DKFZp434G227 (from clone DKFZp434G227)	Unpublished	180	-
32	0	hypothetical protein	54897_at	HG-U95B	AA167714							3.9		2.9	4.7	FLJ31566 fis, clone NT2RP2002211	Unpublished	181	-
33	0	hypothetical protein	57050_at	HG-U95B	AA121987			KIAA1268	3q21.1	3.2	2.8	2.4	2.2	1.7	KIAA1268 protein	Unpublished	182	-
34	0	hypothetical protein	59519_at	HG-U95B	AA210695			KIAA1268	3q21.1	4.1		4	2.2	5.9	KIAA1268 protein	Unpublished	183	-
35	0	hypothetical protein	57694_at	HG-U95B	AI821798							3		2.5	F-box only protein 22	Unpublished	184	-
36	0	hypothetical protein	57898_at	HG-U95B	W06879							2.1		2	F-box only protein 22	Unpublished	185	-

Table 13

										lot 1				lot 2					
										Day 3		Day 7		Day 3	Day 7				
	Cat_tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	AI	DMM	AI	DMM	AI	AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
37	8	hypothetical protein	59036_at	HG-U95B	AA702248							3.5			18.5	FLJ14241 fis, clone OVARC1000533	Unpublished	186	-
38	8	interferon-inducible protein	48884_at	HG-U95B	AI391845	NM_005532	NP_005523	IFI27	14q32	2.9	4			2.1	3.3			187	688
39	8	interferon-inducible protein	52815_at	HG-U95B	AA948319	NM_052942	NP_443174	GBP5	1p22.1	2.4	2.5			4.5		guanylate binding protein 5	Unpublished	188	689
40	10	kinase	46459_at	HG-U95B	AI806723	NM_000293	NP_000284	PHKB	16q12-q13	2			-2.7			phosphorylase kinase, beta	Eur. J. Biochem. 238:374-380 (1996)	189	690
41	10	kinase	48035_at	HG-U95B	AA101125	NM_007203	NP_009134	AKAP2	9q31-q33	6.6		4.4		3	6.4	A kinase (PRKA) anchor protein 2	Unpublished	190	691
42	10	kinase	51085_at	HG-U95B	AW005054	NM_020397	NP_065130	LOC57118	10p13	2.4	3	2.2	5	2.7		CamKI-like protein kinase	Blood 96:3215-3223(2000)	191	692
43	10	kinase	51923_at	HG-U95B	AI769914	NM_021972	NP_068807	SPHK1	17q25.2			2.1			2.5	sphingosine kinase 1	J. Biol. Chem.273:23722-23728 (1998)	192	693
44	10	kinase	58474_at	HG-U95B	W23068	NM_014365	NP_055180	H11	12q24.23			2.3			2.1	protein kinase H11	J. Biol. Chem. 275:25690-25699 (2000)	193	694
45	12	membrane protein	48260_at	HG-U95B	AI452474	NM_021101	NP_066924	CLDN1	3q28-q29	2.4				2.4	3.6	claudin 1	Unpublished :- (1998)	194	695
46	12	membrane protein	50320_g_at	HG-U95B	AI497833	NM_002856	NP_002847	PVRL2	19q13.2-q13.4			2.2		2.2	2.2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	Gene 159:267-272 (1995)	195	696
47	12	membrane protein	51628_at	HG-U95B	AA009692	NM_032048	NP_114437	EMILIN-2	18p11.3	2.1	2.8	3.1	5	2.6		extracellular glycoprotein EMILIN-2 precursor	J. Biol. Chem. 276:12003-12011 (2001)	196	697
48	14	MHC	49203_f_at	HG-U95B	AI329080	NM_018950	NP_084602	HLA-F	6p21.3	2.4	3.1	3.4	2.1		2.8	major histocompatibility complex, class I, F	Unpublished	197	698
49	16	oncogenesis	50388_at	HG-U95B	AA044708	NM_004225	NP_004216	MFHAS1	8p23.1	2.3		2.3	2.6	2.4	2.4	malignant fibrous histiocytoma amplified sequence 1	Cancer Res. 59:511-515 (1999)	198	699
50	16	oncogenesis	52187_at	HG-U95B	AA151346	NM_031458	NP_113646	BAL	3q13-q21	3.5	3.6			2.7	1.6	B aggressive lymphoma gene	Blood 96:4328-4334(2000)	199	700

Table 14



Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Int.1 Day 3 AI	Int.1 Day 3 IMM	Int.1 Day 7 AI	Int.1 Day 7 IMM	Int.2 Day 3 AI	Int.2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
51	17 others	44583_at	HG-U95B	AA603344	NM_015474	NP_056289	SAMHD1	20p1a-q12	6.6	4.3		2.9	6.2		SAM domain and HD domain	Immunol. Lett. 74:221-224 (2000)	200	701
52	17 others	48178_at	HG-U95B	N58274	NM_013399	NP_037531	C18orf3	18q13.3			4.6			1.7	chromosome 18 open reading frame 3	J. Hum. Genet. 44:383-387 (1999)	201	702
53	17 others	48388_at	HG-U95B	AA262083	NM_016072	NP_057156	LOC51026	12p12.1			2.9			2.4	COC4-like protein	Unpublished :- (2002)	202	703
54	17 others	50094_at	HG-U95B	AA102515	NM_004657	NP_004648	SDPR	2q32-q33		2.5	2.3	2.4	4.6	2.7	serum deprivation response (phosphatidylserine-binding protein)	Biochem. J. 269:729-734 (1990)	203	704
55	17 others	50098_at	HG-U95B	AI978251	NM_020375	NP_065108	C12orf5	12p13.3			3.5	2.1	2.3	3.6	chromosome 12 open reading frame 5	Nat. Genet. 28:345-349(2000)	204	705
56	17 others	51235_at	HG-U95B	AI921740	NM_016118	NP_057207	LOC51867	17q36		4.8	3.7	3.7		3.1	NEDD8 ultimate buster-1	Unpublished	205	706
57	17 others	52657_at	HG-U95B	AI038272	NM_058186	NP_478068	C21orf11	21q22.3	2.6	4.6	6.6	3.3		3.7	chromosome 21 open reading frame 11	Unpublished	206	707
58	17 others	52675_at	HG-U95B	AI581142			KIAA1971	15q24.2							ESTs, Weakly similar to T00329 hypothetical protein KIAA0553 [Homo sapiens]	Unpublished	207	-

Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Int.1 Day 3 AI	Int.1 Day 3 IMM	Int.1 Day 7 AI	Int.1 Day 7 IMM	Int.2 Day 3 AI	Int.2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
59	18 P450	47827_at	HG-U95B	AI445492	NM_030622	NP_085125	CYP2S1	19q13.1			2.4	2.5	2.3	2.9	cytochrome P450, subfamily IIS, polypeptide 1	Nature 377:3-174(1995)	208	708

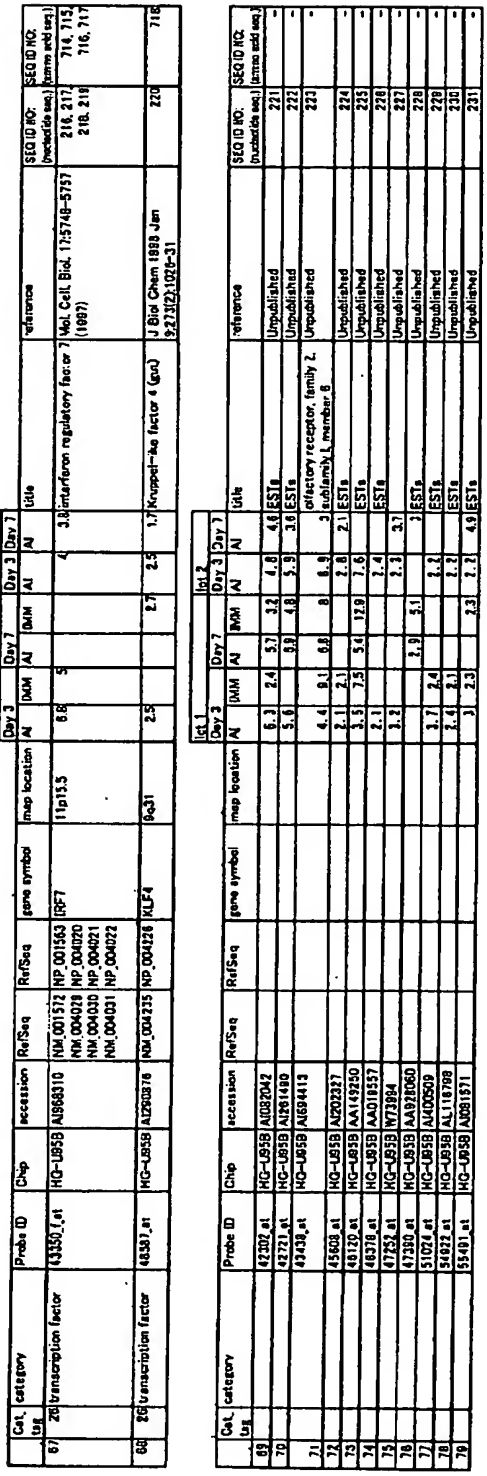
Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Int.1 Day 3 AI	Int.1 Day 3 IMM	Int.1 Day 7 AI	Int.1 Day 7 IMM	Int.2 Day 3 AI	Int.2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
60	20 protein binding protein	48838_s_at	HG-U95B	AI058031	NM_003749	NP_003738	SSH-1	19p13.13	5.4		6.5	8.4	14.8				209	709
61	20 protein binding protein	47900_i_at	HG-U95B	AA805337			IRLB	15q22.1	2.8		3.5	2.2	1.7		c-myc promoter-binding protein	Unpublished	210	-

Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Int.1 Day 3 AI	Int.1 Day 3 IMM	Int.1 Day 7 AI	Int.1 Day 7 IMM	Int.2 Day 3 AI	Int.2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
62	21 proteinase	51972_at	HG-U95B	AA143784	NM_017414	NP_059110	USP18	22q11.21	7.8	7.7			6.8		ubiquitin specific protease 18	J. Biol. Chem. 275:8880-8888 (2000)	211	710

Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Int.1 Day 3 AI	Int.1 Day 3 IMM	Int.1 Day 7 AI	Int.1 Day 7 IMM	Int.2 Day 3 AI	Int.2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
63	24 signal transduction	35039_at	HG-U95B	AW032068	NM_013324	NP_037456	CISH	3p21.3	11.2	12.4	7.2	11	34.5		cytokine inducible SH2-containing protein	Unpublished :- (1997)	212	711
64	24 signal transduction	35107_at	HG-U95B	AI818306	NM_014600	NP_055415	EHD3	2p21	2.2		2.4	2.4	2.4	1.8	EH-domain containing 3	Genomics 63:235-243(2000)	213	712
65	24 signal transduction	50159_s_at	HG-U95B	AA418933										2.1	peptidylprolyl isomerase (cyclophilin)-like 3	Unpublished	214	-

Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Int.1 Day 3 AI	Int.1 Day 3 IMM	Int.1 Day 7 AI	Int.1 Day 7 IMM	Int.2 Day 3 AI	Int.2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
66	25 structural protein	46884_at	HG-U95B	AI961431	NM_015515	NP_056320	HAK1	17q21.1	2.2	2.2	4.4	2.1	2.2	7	type I intermediate filament cytokeratin	Unpublished :- (2002)	215	713

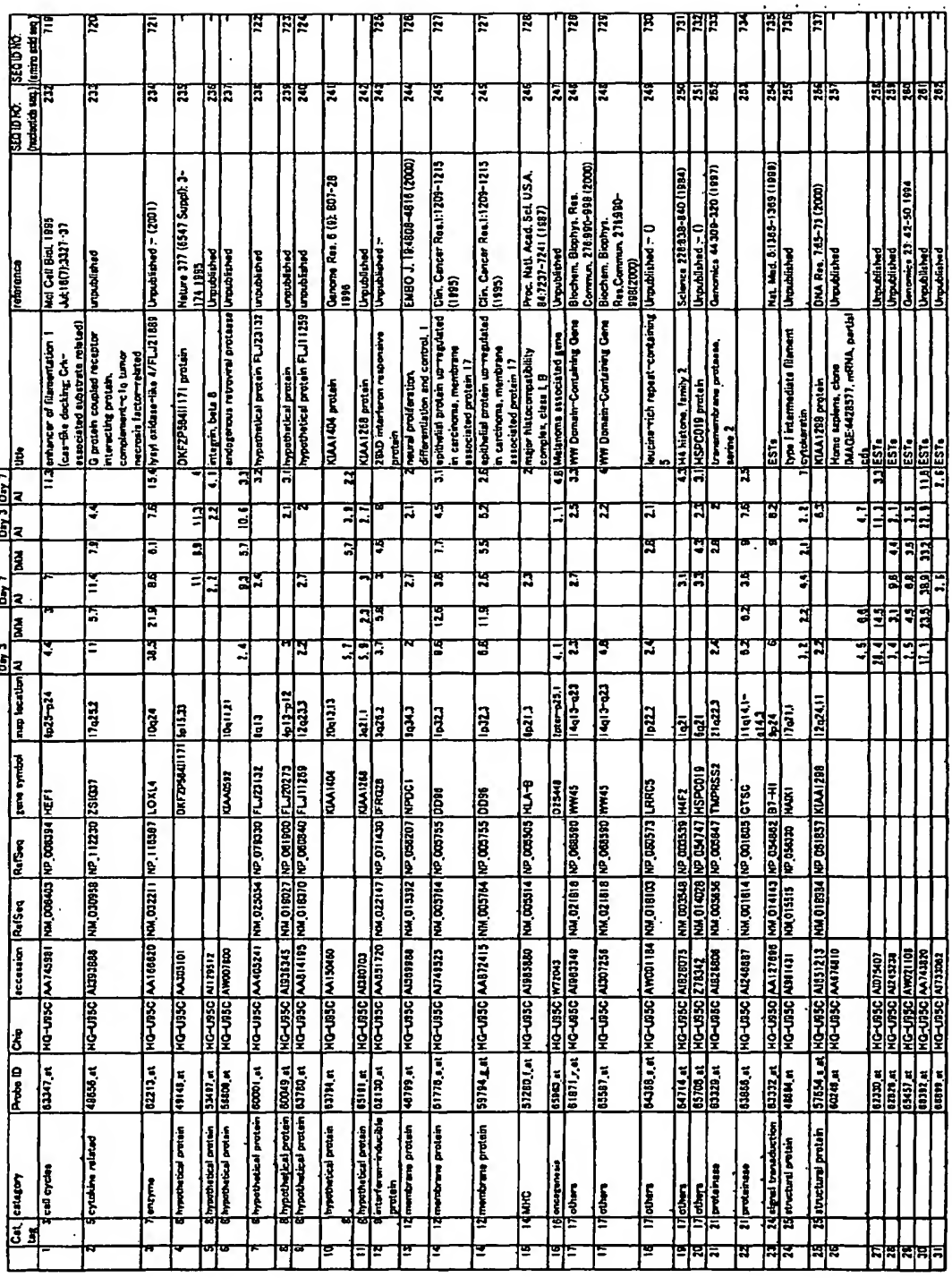
Table 15



	Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Int 1 Day 3 AI	Int 1 Day 7 IMM	Int 1 Day 7 AI	Int 2 Day 3 AI	Int 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
67	26	transcription factor	43350_at	HG-U95B	AI868310	NM_001512 NM_004028 NM_004030 NM_004031	NP_001563 NP_004020 NP_004021 NP_004022	IDF7	11p15.5	6.8	5		4	3.8	interferon regulatory factor 7	Mol. Cell. Biol. 17:5748-5757 (1997)	216, 217, 218, 219	714, 715, 716, 717
68	86	transcription factor	48381_at	HG-U95B	AI290876	NM_004235	NP_004226	KLF4	9q31	2.5		2.7	2.5	1.7	Kruppel-like factor 4 (gut)	J Biol Chem 1998 Jan 9;273(2):1026-31	220	718

	Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Int 1 Day 3 AI	Int 1 Day 7 IMM	Int 1 Day 7 AI	Int 2 Day 3 AI	Int 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
69			42207_at	HG-U95B	AI032042													
70			42721_at	HG-U95B	AI261480					6.3	2.4	5.7	3.2	4.8	ESTs	Unpublished	221	-
			43430_at	HG-U95B	AI694413					5.6		6.8	4.8	5.9	ESTs	Unpublished	222	-
71										4.4	8.1	6.8	8	8.8	olfactory receptor, family 2, subfamily L, member 8	Unpublished	223	-
72			45608_at	HG-U95B	AI202337					2.1	2.1		2.8	2.1	ESTs	Unpublished	224	-
73			46139_at	HG-U95B	AA149250					3.5	7.5	5.4	12.9	7.6	ESTs	Unpublished	225	-
74			46378_at	HG-U95B	AA019557					2.1				2.4	ESTs	Unpublished	226	-
75			47252_at	HG-U95B	W73984					3.2				2.3	ESTs	Unpublished	227	-
76			47380_at	HG-U95B	AA928060							2.9	5.1		3 ESTs	Unpublished	228	-
77			51074_at	HG-U95B	AI400509					3.7	2.4			2.2	ESTs	Unpublished	229	-
78			54022_at	HG-U95B	AL118798					2.4	2.1			2.2	ESTs	Unpublished	230	-
79			55401_at	HG-U95B	AI091671					3	2.3		2.3	2.2	4.9 ESTs	Unpublished	231	-

Table 16



	Cat. No.	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Int.1 Day 3 AI	Int.1 Day 7 AI	Int.1 Day 7 IMM	Int.2 Day 3 AI	Int.2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
1	3	cell cycle	63347_at	HG-U95C	AA745581	NM_006403	NP_006394	HEF1	6p25-p24	4.4	3	7		11.2	enhancer of filamentation 1 (cas-like docking Crk-associated substrate related)	Mol Cell Biol, 1999 Jul;19(7):3327-37	232	719
2	5	cytokine related	40656_at	HG-U95C	AB033868	NM_030938	NP_112230	2510G37	17q25.3	11	5.7	11.4	7.9	4.4	G protein coupled receptor interacting protein, complement-c1q tumor necrosis factor-related	unpublished	233	720
3	7	enzyme	62213_at	HG-U95C	AA166620	NM_032211	NP_115587	LOXL4	10q24	38.5	21.9	8.6	6.1	7.6	13.4	lysyl oxidase-like 4/FLJ21889	Unpublished ~ (2001)	234	721
4	8	hypothetical protein	49148_at	HG-U95C	AA303101			DKFZP564I171	5p15.33			11	8.8	11.3	4	DKFZP564I171 protein	Nature 377 (6547 Suppl): 3-174 1995	235	-
5	8	hypothetical protein	53497_at	HG-U95C	AI129317							2.1		2.2	4.1	integrin, beta 8	Unpublished	236	-
6	8	hypothetical protein	54609_at	HG-U95C	AW007800			KIAA0592	10q11.21			9.2	5.7	10.6	3.1	endogenous retroviral protease	Unpublished	237	-
7	8	hypothetical protein	60001_at	HG-U95C	AA405241	NM_025054	NP_079330	FLJ23132	8q13			2.4			3.2	hypothetical protein FLJ23132	unpublished	238	722
8	8	hypothetical protein	60049_at	HG-U95C	AB038245	NM_018927	NP_061800	FLJ20275	9p13-p12	3				2.1	3.1	hypothetical protein	unpublished	239	723
9	8	hypothetical protein	63760_at	HG-U95C	AA814195	NM_018370	NP_060840	FLJ11259	12q23.3	2.2		2.7		2		hypothetical protein FLJ11259	unpublished	240	724
10	8	hypothetical protein	63794_at	HG-U95C	AA130460			KIAA1404	10q13.13		5.1		5.2	2.8	2.2	KIAA1404 protein	Genome Res. 6 (9): 807-28 1996	241	-
11	8	hypothetical protein	65101_at	HG-U95C	AB30703			KIAA1268	3q21.1	5.9	2.3	3		2.7		KIAA1268 protein	Unpublished	242	-
12	8	interferon-inducible protein	62130_at	HG-U95C	AA831720	NM_022147	NP_071430	IFRG28	3q26.2	3.7	9.8	3	4.8	6		28kD interferon responsive protein	Unpublished ~	243	725
13	12	membrane protein	40799_at	HG-U95C	AI659988	NM_015392	NP_056207	NPDC1	9q34.3	2		2.7		2.1	2	neural proliferation, differentiation and control, 1	EMBO J. 19:4808-4818 (2000)	244	726
14	12	membrane protein	61770_s_at	HG-U95C	AI749323	NM_005764	NP_005755	DD96	1p32.3	9.6	12.6	3.6	7.7	4.5	3.1	epithelial protein up-regulated in carcinoma, membrane associated protein 17	Clin. Cancer Res.1:1205-1215 (1995)	245	727
15	12	membrane protein	59794_g_at	HG-U95C	AA872415	NM_005764	NP_005755	DD96	1p32.3	8.6	11.9	2.6	5.5	5.2	2.6	epithelial protein up-regulated in carcinoma, membrane associated protein 17	Clin. Cancer Res.1:1205-1215 (1995)	245	727
16	14	MHC	37280_f_at	HG-U95C	AI985880	NM_005514	NP_005505	HLA-B	6p21.3			2.3			2	major histocompatibility complex, class I, B	Proc. Natl. Acad. Sci. U.S.A. 84:7237-7241 (1987)	246	728
17	16	oncogenesis	65963_at	HG-U95C	W72043			D15S48	15q14-q21.1	4.1			1.1	4.8		Melanoma associated gene	Unpublished	247	-
18	17	others	61871_r_at	HG-U95C	AI983348	NM_021818	NP_068580	WW45	14q13-q23	2.3		2.7		2.5	3.3	WW Domain-Containing Gene	Biochem. Biophys. Res. Commun. 276:890-898 (2000)	248	728
19	17	others	63587_at	HG-U95C	AI207258	NM_021818	NP_068580	WW45	14q13-q23	4.8				2.2	4	WW Domain-Containing Gene	Biochem. Biophys. Res.Commun. 276:890-898(2000)	248	729
20	17	others	64388_r_at	HG-U95C	AW001184	NM_018103	NP_060573	LRRC5	11p12.2	2.4		2.8		2.1		leucine-rich repeat-containing 5	Unpublished ~ U	249	730
21	17	others	64714_at	HG-U95C	AI828073	NM_003539	NP_003530	H4F2	1q21			3.1			4.5	H4 histone, family 2	Science 278:838-840 (1984)	250	731
22	17	others	65708_at	HG-U95C	Z78342	NM_014078	NP_054747	HSPC019	6q21			3.3	4.3	2.3	3.1	HSPC019 protein	Unpublished ~ U	251	732
23	21	protease	63329_at	HG-U95C	AI823806	NM_005836	NP_005647	TMPRSS2	21q22.3	2.4			2.8	2		transmembrane protease, serine 2	Genomics 44:309-320 (1997)	252	733
24	21	protease	63868_at	HG-U95C	AI246887	NM_001814	NP_001805	CTSC	11q14.1-q14.3	8.2	8.2	3.6	9	7.6	2.5			253	734
25	24	signal transduction	63332_at	HG-U95C	AA127986	NM_014143	NP_054862	B7-H1	9p24	6			9	8.2		ESTs	Nat. Med. 8:1365-1369 (1998)	254	735
26	25	structural protein	48804_at	HG-U95C	AB011431	NM_015515	NP_056320	HADI	17q21.1	1.1	2.2	4.5	2.1	1.1	7	hyp I intermediate filament cytokeratin	Unpublished	255	736
27	25	structural protein	57154_s_at	HG-U95C	AI351213	NM_018334	NP_060804	KIAA1288	12q24.11	2.2				8.3		KIAA1288 protein	DNA Res. 7:65-73 (2000)	256	737
28			60248_at	HG-U95C	AA478410					4.9	9.8			4.2		Homo sapiens, clone IMAGE:4428577, mRNA, partial cds	Unpublished	257	-
29			62230_at	HG-U95C	AI075407					28.4	14.5			11.3	3.3	ESTs	Unpublished	258	-
30			62878_at	HG-U95C	AI219328					3.4	3.1	9.8	4.4	2.1		ESTs	Unpublished	259	-
31			63457_at	HG-U95C	AW021100					1.5	4.5	6.8	3.9	1.2		ESTs	Genomics 23: 42-50 1994	260	-
32			63892_at	HG-U95C	AA743820					11.1	23.5	38.9	31.2	11.1	11.8	ESTs	Unpublished	261	-
33			64899_at	HG-U95C	AI733062							2.5			2.6	ESTs	Unpublished	262	-

Table 17

Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 3 IMM	lot 1 Day 7 AI	lot 1 Day 7 IMM	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
1	7 enzyme	75624_at	HG-U95D	R45082	NM_001111, NP_001102, NM_018840, NP_061855, NM_013841, NP_038856	ADAR	1q21.1-q21.2	2.8					2		adenosine deaminase, RNA-specific, ADAR isoform e-c	Proc. Natl. Acad. Sci. U.S.A. 91:11457-11461 (1994)	263,264,265	738, 739, 740
2	7 enzyme	79837_at	HG-U95D	AA087417	NM_014080	NP_054789	DUOX2	15q15.3-q21	2.2	2.6	5.7		2.5		dual oxidase 2	Unpublished :- (2000)	266	741
3	7 enzyme	81866_at	HG-U95D	AI199418	NM_021105	NP_066928	PLSCR1	3q23	3.3				3.3		phospholipid scramblase 1	J. Biol. Chem. 272 (29), 18240-18244 (1997)	267	742
4	8 hypothetical protein	75423_at	HG-U95D	AI245770					2.1				2.2	2.8	Homo sapiens mRNA; cDNA DKFZp564N1164 (from clone DKFZp564N1164)		268	
5	8 hypothetical protein	75857_at	HG-U95D	W60832					3.6	3.2	3.4	4.3	3.1	2.5	Homo sapiens cDNA FLJ12334 fis, clone PROST2003416		269	
6	8 hypothetical protein	82008_at	HG-U95D	AA189927							2.1		11.7	4.2	Homo sapiens cDNA: FLJ21270 fis, clone COL01749		270	
7	8 hypothetical protein	91851_at	HG-U95D	AI051434					3.5			2.1	2.3		Homo sapiens cDNA FLJ12138 fis, clone MAMMA1000312		271	
8	24 signal transduction	88890_at	HG-U95D	AW001845	NM_002483	NP_002474	NK2	21q22.3	9.6	9.8			3.2		myoviroma (influenza) resistance; homolog of murine	Mol. Cell. Biol. 9:5062-5072(1989)	272	743
9		71157_at	HG-U95D	AI819178					4.4	4	3.5	5.8	3.8		EST		273	
10		74988_at	HG-U95D	AW029482					4.3				8.5		EST		274	
11		75080_at	HG-U95D	AI735440							2.6				EST		275	
12		80077_at	HG-U95D	AI765608					3		3.8		7.7	4.4	EST		276	
13		80878_at	HG-U95D	AA113406					2.2			3.7	2.1		EST		277	

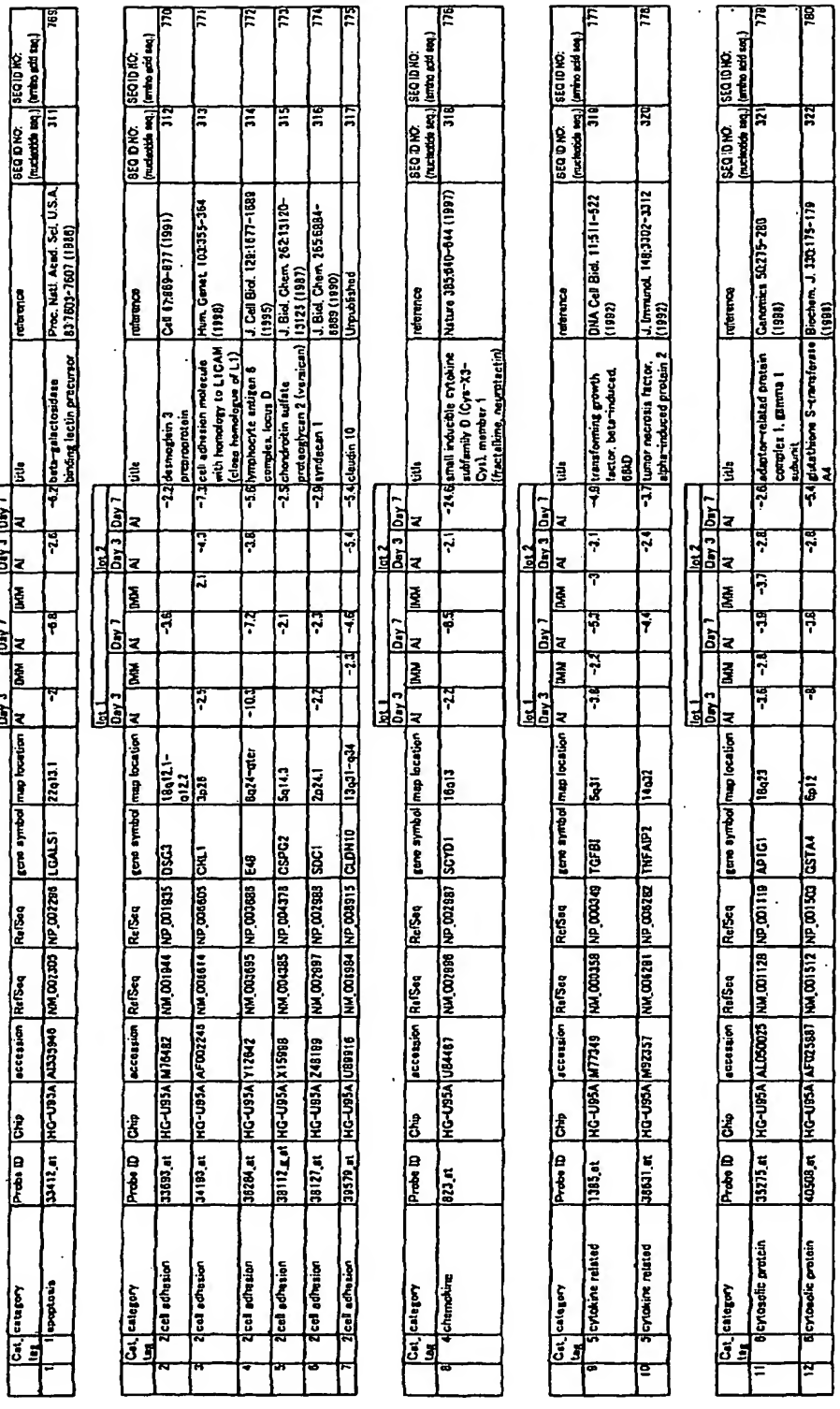
Table 18

	Cat_1	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lgt 1 Day 3 AI	lgt 1 Day 3 DMM	lgt 2 Day 7 AI	lgt 2 Day 7 DMM	lgt 2 Day 3 AI	lgt 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
1	2	cell adhesion	90421_at	HG-U95E	AA633203	NM_033253	NP_150280	EPS111	13q13.3	7.2	9.9		3.4	9.4		epithelial stromal interaction 1 (breast)	Unpublished ~ 0	278	744
2	4	chemokine	90189_at	HG-U95E	AI928371	NM_006072	NP_006063	SCYA26	7q11.2	28.3	18.1	30.4	35.1	16.7	29.8	small inducible cytokine subfamily A (Cys-Cys), member 26 (eotaxin-3)	J. Exp. Med. 185:1163-1172(1997)	278	745
3	7	enzyme	72882_at	HG-U95E	AA705651	NM_005504	NP_005493	BCAT1	12p12.1			2.7	3.4	10.5	3.7	Homo sapiens cDNA FLJ21270 fis, clone COL01749/ branched chain aminotransferase 1, cytosolic		280	746
4	7	enzyme	77749_at	HG-U95E	AB460936	NM_014314	NP_055129	RIG-I	9p12	3.8	3.4	5.1	6.4	2.3	RNA helicase	Thesis ~ (1997)	281	747
5	7	enzyme	77751_at	HG-U95E	AB567061	NM_004751	NP_004742	GCNT3	15q21.3		2.5	3.5		2	glucosaminyl (N-acetyl) transferase 3, mucin type	J. Biol. Chem.274:3215-3221 (1999)	282	748
6	7	enzyme	90682_at	HG-U95E	AI340262	NM_002535, NM_016817	NP_002526, NP_058197	OAS2	12q24.2	4.8	10.2			4.1		2'-5'oligoadenylate synthetase 2, isoform p69, isoform p71	EMBO J. 8:1273-1280 (1987)	283, 284	749, 750
7	8	hypothetical protein	87328_at	HG-U95E	AA610377	NM_022837	NP_073148	FLJ22833				3.6	3.7	6.1	4.2	hypothetical protein FLJ22833	Unpublished ~ 0	285	751
8	8	hypothetical protein	86582_at	HG-U95E	AA779704					3.1				2.8		Homo sapiens cDNA FLJ11138 fis, clone MAMMA1000312		286	-
9	8	hypothetical protein	72887_at	HG-U95E	AW024610							2.8		2.3		Homo sapiens mRNA; cDNA DKFZp434G227 (from clone DKFZp434G227)		287	-
10	8	hypothetical protein	72900_s_at	HG-U95E	AA199856							4.2	3.9	3.6	18.8	5.3	Homo sapiens cDNA FLJ21270 fis, clone COL01749		288	-
11	8	hypothetical protein	77546_at	HG-U95E	AI859144							4.3	5.8	2.6	5.3	9.8	KIAA1127	DNA Res. 8 (5), 319-336 (1999)	289	-
12	8	hypothetical protein	80826_at	HG-U95E	AA808114							4.2	8.1	5.3	7.2	2	Homo sapiens cDNA FLJ25184 fis, clone CBR09423		290	-
13	8	hypothetical protein	83376_at	HG-U95E	AB16814	NM_017742	NP_060212	FLJ20281	18q21.32			2.1			2.6	hypothetical protein FLJ20281	DNA Res. 7:347-355(2000)	291	752
14	8	hypothetical protein	83541_at	HG-U95E	AB43912	NM_018283	NP_060753	KIAA1685	2p14.1			2.6			2	KIAA1685 protein	Unpublished ~ (1)	292	753
15	8	hypothetical protein	89255_at	HG-U95E	AB03946							3.5	7		2.4	Homo sapiens cDNA FLJ11576 fis, clone HEMBA1003548		293	-
16	8	hypothetical protein	86834_at	HG-U95E	AB84061							2.7			3.1	ESTs, Weakly similar to T22914 hypothetical protein F58E10.4 ~ Caenorhabditis elegans [C.elegans]		294	-
17	8	hypothetical protein	89902_at	HG-U95E	AW02878	NM_024738	NP_079014	FLJ21415	12q24.21			3.4			2.7	hypothetical protein FLJ21415	Unpublished ~ (2000)	295	754
18	8	hypothetical protein	91420_at	HG-U95E	AA558752	NM_023080	NP_075558	FLJ20989				3.4			2.1	hypothetical protein FLJ20989	Unpublished ~ 0	296	755
19	9	interferon-inducible protein	84893_at	HG-U95E	AU448168	NM_080657	NP_542388	vipirin	2p15.3	14.8	13.5	2.7	6.6	15.4		Homo sapiens vipirin (cig5), mRNA	Unpublished ~ (2001)	297	756
20	12	membrane protein	77660_at	HG-U95E	AI889132	NM_021101	NP_066924	CLDN1	3q28~q29			2.6			5.4			298	757
21	12	membrane protein	86507_at	HG-U95E	AI832218	NM_031308	NP_112598	EPPK1				2.8	3.6		3.2	epiplakin 1	J. Biol. Chem.276:13340-13347 (2001)	298	758
22	16	oncogenesis	89619_at	HG-U95E	AU070955	NM_031458	NP_113648	BAL	3q13	3.5	3.1		2.2	3.1	2.4	B aggressive lymphoma gene	Blood 98:4320-4334(2000)	300	759
23	16	oncogenesis	87816_g_at	HG-U95E	AU079308	NM_004225	NP_004216	MFHAS1	8p23.1	3		3.4	3.1	3.5	2.7	malignant fibrous histiocytoma amplified sequence 1	Cancer Res.59:511-515 (1999)	301	760
24	16	oncogenesis	89651_at	HG-U95E	AW003551	NM_004225	NP_004216	MASL1	8p23.1			4.3		3.2	4.2	MFH-amplified sequences with leucine-rich tandem repeats 1 (MASL1)	Cancer Res.59:511-515 (1999)	301	760
25	17	others	80675_at	HG-U95E	AI960036	NM_000618	NP_000609	IGF1	12q23	2.2				2.3		ribosomal protein L4	Biochim Biophys.	302	761
26	17	others	85090_at	HG-U95E	AI354809	NM_012153	NP_036285	EHF	11p12	2.3				3.3		3ets homologous factor	Acta 1218:472-478 (1993) Biochem. Biophys. Res.Commun. 284:119-128 (1993)	303	762

Table 19

25	17	others	85092_g_at	HG-U95E	AI354809	NM_012153	NP_036285	EIF	11p12		2.3	2.1	3.3	7	beta homologous factor	Biochem. Biophys. Res.Commun. 264:119-126 (1999)	303	742
26	17	others	89320_at	HG-U95E	AA308288	NM_032390	NP_115766	NGFK	2q14.2			2.9	2.1	3.4	nucleolar protein interacting with the FHA domain of pKi-67	J. Biol. Chem.276:25186-25191 (2001)	304	743
27	20	protein binding protein	89338_at	HG-U95E	AA102335	NM_025151	NP_079427	rab11-FIP1	8p11.22			4.4		14.6	Rab effector protein Rab-interacting recycling protein/rab11-family interacting protein 1	J. Biol. Chem.276:38067-38075 (2001)	305	744
28	24	signal transduction	87125_at	HG-U95E	AI925166	NM_024865	NP_078941	TBLR1	3q23		2.8		4.4		nuclear receptor co-repressor/HDAC3 complex subunit	Exp. Hematol.28:1286-1298 (2000)	306	745
29	27	transporter	34759_at	HG-U95E	U68494	NM_005828	NP_005819	SLC1A5	19q13.3			2.5		2.9	Hoc647 mRNA sequence(SOLUTE CARRIER FAMILY 1 (NEUTRAL AMINO ACID TRANSPORTER), MEMBER 5)	J. Virol. 73, 4470-4474 (1999)	307	746
30	27	transporter	87880_s_at	HG-U95E	AW018409	NM_018354	NP_057438	SLC21A12	1q43	2.7		2.7		2.8	solute carrier family 21 (organic anion transporter), member 12	Unpublished :- (2001)	308	747
31	27	transporter	88817_at	HG-U95E	N21316	NM_012434	NP_036566	SLC17A5	6q14-q15			2.7		2.3	solute carrier family 17 (anion/sugar transporter), member 5	Nat. Genet. 23:462-465 (1999)	309	748
32			87357_at	HG-U95E	H70885						2.6		2.1		drosophila) homolog 1		310	

Table 20



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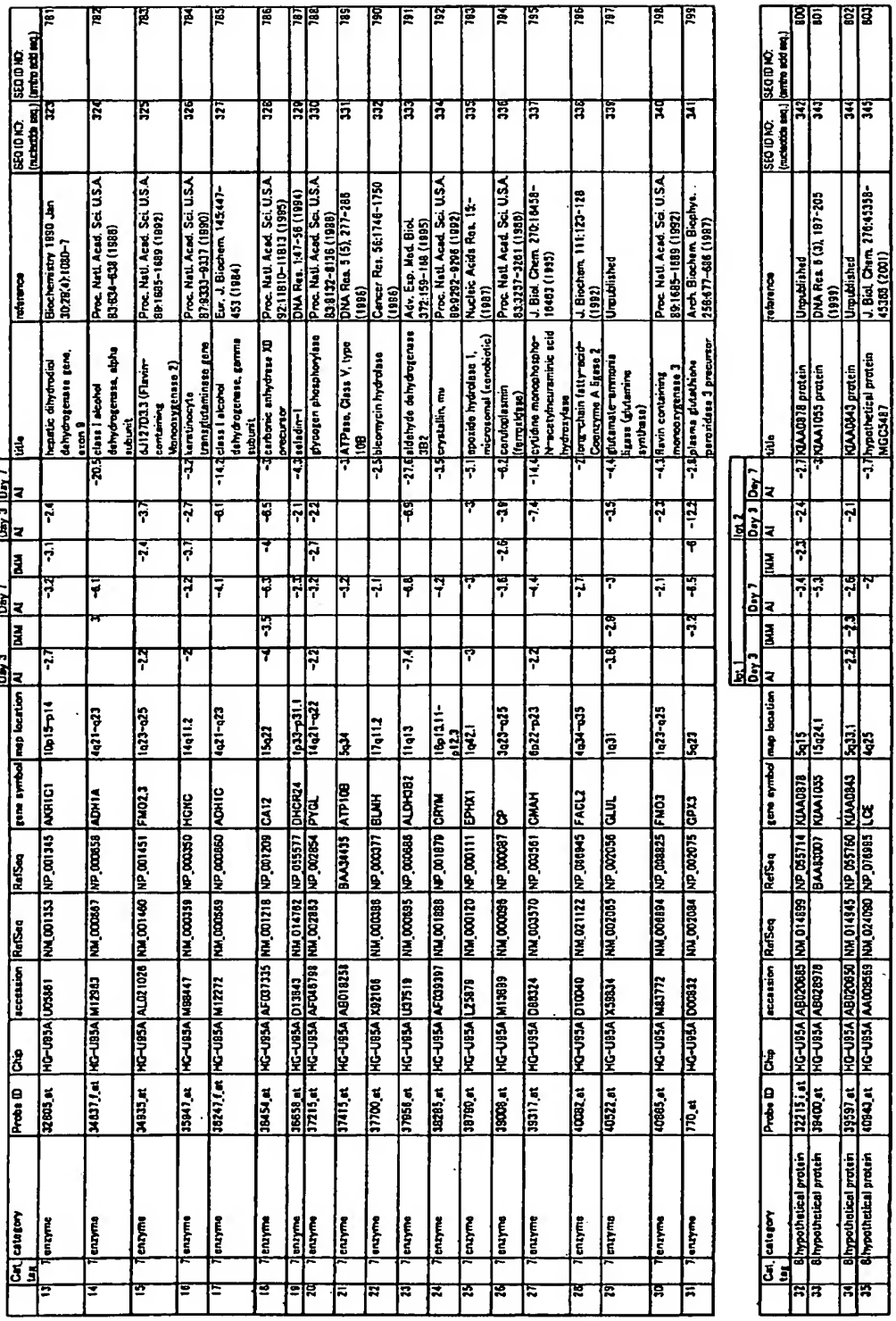
1	1	apoptosis	33412_at	HG-U95A	AI333946	NM_002309	NP_002298	LGALS1	22q13.1	-2		-6.8	-2.6	-6.2	beta-galactosidase binding lectin precursor	Proc. Natl. Acad. Sci. U.S.A. 83:7603-7607 (1986)	311	765
2	2	cell adhesion	33693_at	HG-U95A	M76482	NM_001944	NP_001935	DSG3	18q12.1-q12.2		-3.6			-2.2	desmoglein 3 precursor protein	Cell 67:69-877 (1991)	312	770
3	2	cell adhesion	34193_at	HG-U95A	AF002248	NM_006614	NP_006605	CHL1	3p26	-2.5		2.1	-4.3	-7.3	cell adhesion molecule with homology to L1CAM (close homologue of L1)	Hum. Genet. 102:355-364 (1998)	313	771
4	2	cell adhesion	36284_at	HG-U95A	Y12842	NM_003895	NP_003886	E48	8q24-qter	-10.3	-7.2		-3.8	-5.8	lymphocyte antigen 6 complex, locus D	J. Cell Biol. 128:1677-1688 (1995)	314	772
5	2	cell adhesion	38112_g_at	HG-U95A	X15998	NM_004385	NP_004376	CSPG2	5q14.3		-2.1			-2.5	chondroitin sulfate proteoglycan 2 (versican)	J. Biol. Chem. 262:13120-13125 (1987)	315	773
6	2	cell adhesion	38127_at	HG-U95A	Z48199	NM_002997	NP_002988	SDC1	2p24.1	-2.2	-2.3			-2.9	syndecan 1	J. Biol. Chem. 265:6884-6889 (1990)	316	774
7	2	cell adhesion	39579_at	HG-U95A	U89916	NM_006984	NP_008915	CLDN10	13q31-q34		-2.3	-4.6	-5.4	-5.4	claudin 10	Unpublished	317	775
8	4	chemokine	823_at	HG-U95A	U64867	NM_002988	NP_002987	SCYD1	16q13	-2.2	-6.5		-2.1	-24.8	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)	Nature 385:640-644 (1997)	318	776
9	5	cytokine related	1385_at	HG-U95A	M77349	NM_000358	NP_000349	TGFBI	5q31	-3.8	-2.2	-5.2	-3	-2.1	transforming growth factor, beta-induced, 68kD	DNA Cell Biol. 11:511-522 (1992)	319	777
10	5	cytokine related	38631_at	HG-U95A	M92357	NM_006281	NP_006182	TNFAIP2	14q32			-4.4		-2.4	tumor necrosis factor, alpha-induced protein 2	J. Immunol. 148:3302-3312 (1992)	320	778
11	6	cytosolic protein	35275_at	HG-U95A	AL050025	NM_001128	NP_001119	AP1G1	16q23	-3.6	-2.8	-3.9	-3.7	-2.8	adaptor-related protein complex 1, gamma 1 subunit	Genomics 50:275-280 (1998)	321	779
12	6	cytosolic protein	40508_at	HG-U95A	AF025887	NM_001512	NP_001503	GSTA4	6p12	-8		-3.8		-2.8	-5.4	glutathione S-transferase A4	Biochem. J. 330:175-179 (1998)	322	780

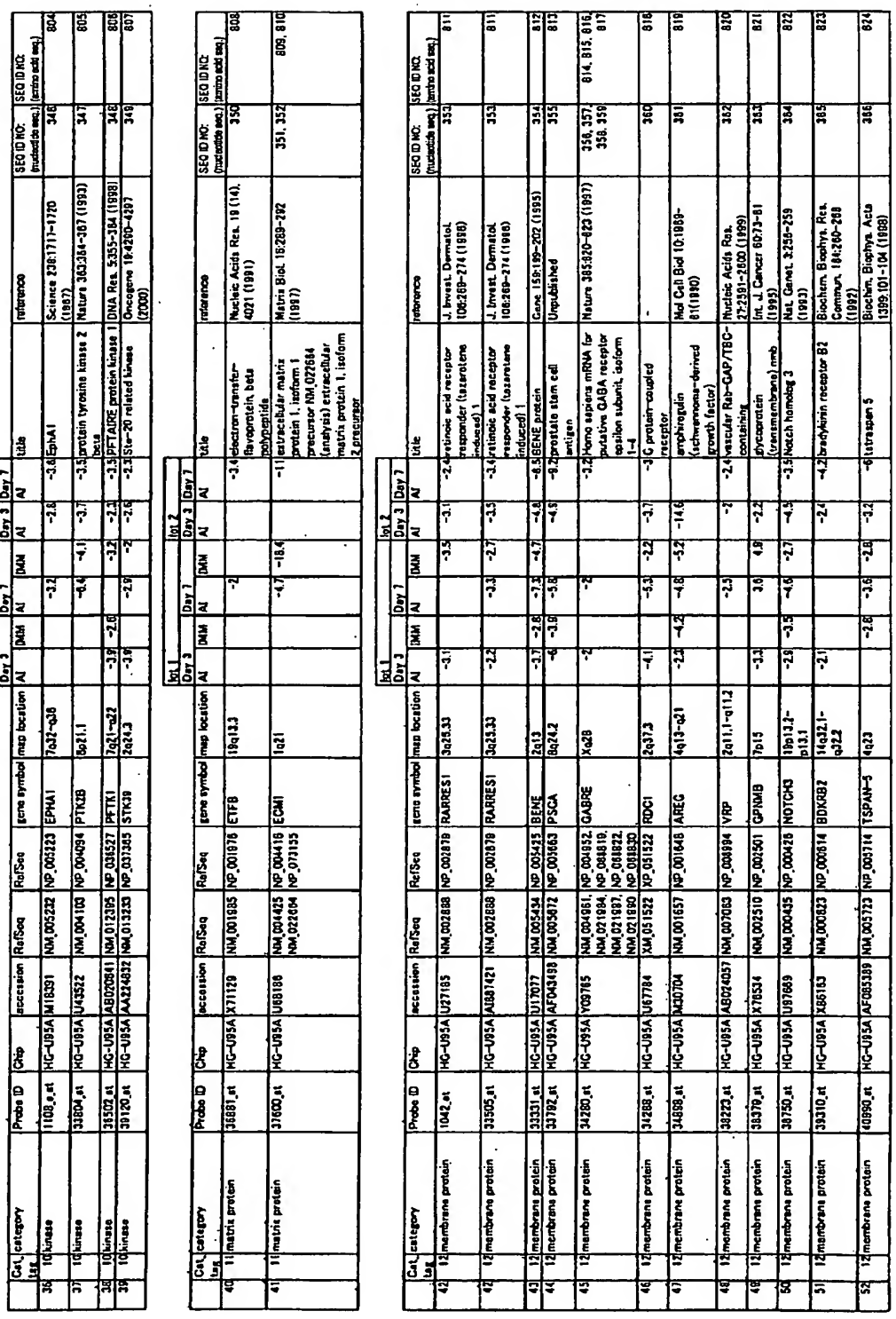
Table 21



	Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lgt 1 Day 3 AI	lgt 1 Day 7 IMM	lgt 1 Day 7 AI	lgt 2 Day 3 IMM	lgt 2 Day 3 AI	lgt 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
13	7	enzyme	32603_at	HG-U95A	U05861	NM_001353	NP_001345	AKR1C1	10p15-p14	-2.7		-3.2	-3.1	-2.4		hepatic dihydrodiol dehydrogenase gene, exon 9	Biochemistry 1990 Jan 30;29(4):1030-7	323	781
14	7	enzyme	34837_at	HG-U95A	M12963	NM_000667	NP_000658	ADH1A	4q21-q23		3	-6.1			-20.5	class I alcohol dehydrogenase, alpha subunit	Proc. Natl. Acad. Sci. U.S.A. 83:834-838 (1986)	324	782
15	7	enzyme	34835_at	HG-U95A	AL021026	NM_001460	NP_001451	FMO2.3	1q23-q25	-2.2		-2.4		-3.7		6J1170313 (Flavin-containing Monooxygenase 2)	Proc. Natl. Acad. Sci. U.S.A. 89:1685-1689 (1992)	325	783
16	7	enzyme	35947_at	HG-U95A	M88447	NM_000339	NP_000330	HGNC	14q11.2	-2		-3.2	-3.7	-2.7	-3.2	keratinocyte lysyltransferase gene	Proc. Natl. Acad. Sci. U.S.A. 87:9333-9337 (1990)	326	784
17	7	enzyme	35247_f_at	HG-U95A	M12272	NM_000669	NP_000660	ADH1C	4q21-q23			-4.1		-6.1	-14.2	class I alcohol dehydrogenase, gamma subunit	Eur. J. Biochem. 145:447-453 (1984)	327	785
18	7	enzyme	38458_at	HG-U95A	AF031335	NM_001218	NP_001209	CA12	15q22	-4	-3.5	-6.3	-4	-6.5	-3	carbonic anhydrase XII precursor	Proc. Natl. Acad. Sci. U.S.A. 92:11810-11813 (1995)	328	786
19	7	enzyme	36658_at	HG-U95A	D13843	NM_014762	NP_055577	DHCR24	1p33-p31.1			-2.3		-2.1	-4.3	seladin-1	DNA Res. 1:47-56 (1994)	329	787
20	7	enzyme	37215_at	HG-U95A	AF046788	NM_002853	NP_002844	PYGL	14q21-q22	-2.2		-3.2	-2.7	-2.2		glycogen phosphorylase	Proc. Natl. Acad. Sci. U.S.A. 83:8132-8136 (1986)	330	788
21	7	enzyme	37415_at	HG-U95A	AB018258		BAA34435	ATP10B	5q34			-3.2			-3	ATPase, Class V, type 10B	DNA Res. 5:(5), 277-286 (1998)	331	789
22	7	enzyme	37700_at	HG-U95A	X92106	NM_000388	NP_000377	BLMH	17q11.2			-2.1			-2.5	bleomycin hydrolase	Cancer Res. 56:1746-1750 (1996)	332	790
23	7	enzyme	37958_at	HG-U95A	U37519	NM_000695	NP_000686	ALDH3B2	11q13	-7.4		-6.8		-6.9	-27.6	aldehyde dehydrogenase 3B2	Adv. Exp. Med. Biol. 372:159-168 (1995)	333	791
24	7	enzyme	38265_at	HG-U95A	AF039397	NM_001888	NP_001879	CPYM	18p13.11-p12.3			-4.2			-3.9	crystallin, mu	Proc. Natl. Acad. Sci. U.S.A. 89:9292-9296 (1992)	334	792
25	7	enzyme	38760_at	HG-U95A	L25878	NM_000120	NP_000111	EPHX1	1q42.1	-3		-3		-3	-3.1	lipoxide hydrolase 1, microsomal (xenobiotic)	Nucleic Acids Res. 12:- (1987)	335	793
26	7	enzyme	39008_at	HG-U95A	M13699	NM_000098	NP_000087	CP	3q23-q25			-3.6	-2.6	-3.9	-6.2	ceruloplasmin (ferroxidase)	Proc. Natl. Acad. Sci. U.S.A. 83:3237-3241 (1986)	336	794
27	7	enzyme	39317_at	HG-U95A	D88324	NM_003370	NP_003361	CMAH	6p22-p23	-2.2		-4.4		-7.4	-14.4	cytidine monophospho-N-acetylneuraminic acid hydroxylase	J. Biol. Chem. 270:18458-18463 (1995)	337	795
28	7	enzyme	40082_at	HG-U95A	D10040	NM_021122	NP_066945	FACL2	4q34-q35			-2.7			-2	long-chain fatty-acid-Coenzyme A ligase 2	J. Biochem. 111:123-128 (1992)	338	796
29	7	enzyme	40322_at	HG-U95A	X58834	NM_002065	NP_002056	GLUL	1q31		-3.8	-2.8	-3	-3.5	-4.4	glutamate-ammonia ligase (glutamine synthase)	Unpublished	339	797
30	7	enzyme	40885_at	HG-U95A	M83772	NM_006894	NP_008825	FMO3	1q23-q25			-2.1		-2.3	-4.3	flavin containing monooxygenase 3	Proc. Natl. Acad. Sci. U.S.A. 89:1685-1689 (1992)	340	798
31	7	enzyme	770_at	HG-U95A	D00632	NM_002084	NP_002075	GPX3	5q23			-3.2	-6	-12.2	-2.8	plasma glutathione peroxidase 3 precursor	Arch. Biochem. Biophys. 258:477-486 (1987)	341	799

	Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lgt 1 Day 3 AI	lgt 1 Day 7 IMM	lgt 1 Day 7 AI	lgt 2 Day 3 IMM	lgt 2 Day 3 AI	lgt 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
32	8	hypothetical protein	32215_i_at	HG-U95A	AB020685	NM_014899	NP_055714	KIAA0878	5q15			-3.4	-2.2	-2.4	-2.7	KIAA0878 protein	Unpublished	342	800
33	8	hypothetical protein	39400_at	HG-U95A	AB028978		BAA83007	KIAA1055	15q24.1			-5.3			-3	KIAA1055 protein	DNA Res. 5 (3), 187-205 (1998)	343	801
34	8	hypothetical protein	39597_at	HG-U95A	AB020950	NM_014945	NP_055760	KIAA0843	5q33.1		-2.2	-2.3	-2.6	-2.1		KIAA0843 protein	Unpublished	344	802
35	8	hypothetical protein	40943_at	HG-U95A	AA009869	NM_024080	NP_076985	LOC	4q25			-2			-3.7	hypothetical protein MGC3487	J. Biol. Chem. 276:45358-45363 (2001)	345	803

Table 22



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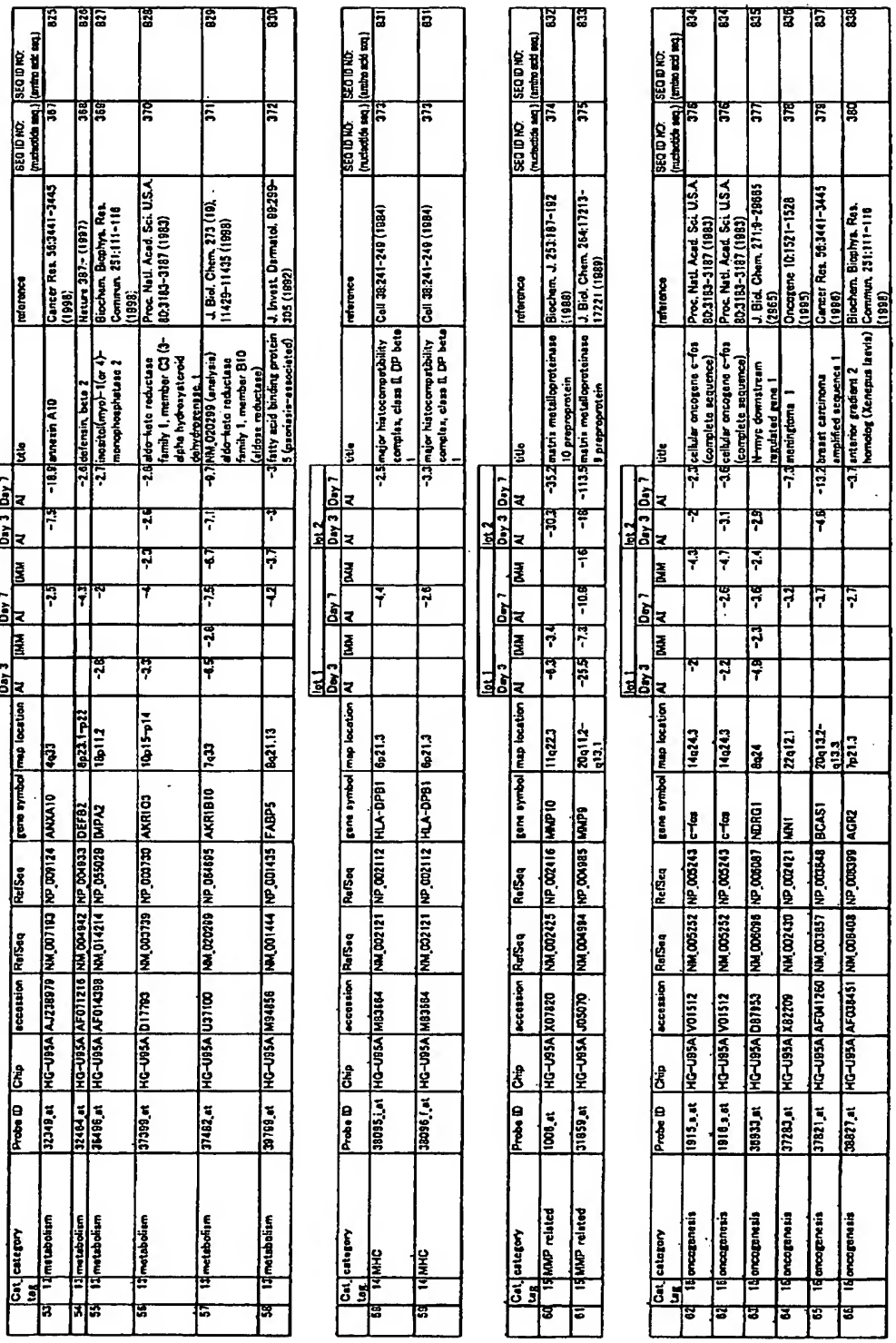
36	10	kinase	11108_s_at	HG-U95A	M18391	NM_005232	NP_005223	EPHA1	7q32-q36			-3.2		-2.8	-3.8	EphA1	Science 236:1711-1720 (1987)	346	804
37	10	kinase	33804_at	HG-U95A	U43522	NM_004103	NP_004094	PTK2B	8p21.1			-6.4	-4.1	-3.7	-3.5	protein tyrosine kinase 2 beta	Nature 363:364-367 (1993)	347	805
38	10	kinase	31502_at	HG-U95A	AB020841	NM_012395	NP_036527	PFTK1	7q21-q22	-3.9	-2.6	-3.2		-2.3	-3.5	PFTAIRE protein kinase 1	DNA Res. 5:355-364 (1998)	348	806
39	10	kinase	39120_at	HG-U95A	AA224832	NM_013233	NP_037365	STK39	2q24.3	-3.9		-2.9	-2	-2.6	-2.3	Ste-20 related kinase	Oncogene 19:4260-4267 (2000)	349	807
40	11	matrix protein	36681_at	HG-U95A	X71129	NM_001985	NP_001976	ETFB	19q13.3			-2			-3.4	electron-transfer-flavoprotein, beta polypeptide	Nucleic Acids Res. 19:(14), 4021 (1991)	350	808
41	11	matrix protein	37600_at	HG-U95A	U68186	NM_001425 NM_022654	NP_004416 NP_073155	ECM1	1q21			-4.7	-18.4		-11	extracellular matrix protein 1, isoform 1 precursor NM_022664 (analysis) extracellular matrix protein 1, isoform 2 precursor	Matrix Biol. 16:269-282 (1997)	351, 352	809, 810
42	12	membrane protein	1042_at	HG-U95A	U27185	NM_002888	NP_002879	RARRES1	3q25.33	-3.1		-3.5		-3.1	-2.4	retinoic acid receptor responder (tazarotene induced) 1	J. Invest. Dermatol. 106:269-274 (1996)	353	811
42	12	membrane protein	33505_s_at	HG-U95A	AI887421	NM_002888	NP_002879	RARRES1	3q25.33	-2.2		-3.3	-2.7	-3.5	-3.4	retinoic acid receptor responder (tazarotene induced) 1	J. Invest. Dermatol. 106:269-274 (1996)	353	811
43	12	membrane protein	33331_at	HG-U95A	U17077	NM_005434	NP_005425	BENE	2q13	-3.7	-2.8	-7.3	-4.7	-4.8	-6.5	BENE protein	Gene 159:199-202 (1995)	354	812
44	12	membrane protein	31782_at	HG-U95A	AF043498	NM_005672	NP_005663	PSCA	8q24.2	-6	-3.8	-5.8		-4.8	-9.2	prostate stem cell antigen	Unpublished	355	813
45	12	membrane protein	34280_at	HG-U95A	Y09765	NM_004961, NM_021984, NM_021987, NM_021990	NP_004952, NP_068819, NP_068822, NP_068830	GABRE	Xq28	-2	-2				-3.2	Homo sapiens mRNA for putative GABA receptor epsilon subunit, isoform 1-4	Nature 365:320-323 (1997)	356, 357, 358, 359	814, 815, 816, 817
46	12	membrane protein	34288_at	HG-U95A	U67784	XM_051522	XP_051522	RDC1	2q37.3	-4.1	-5.3	-2.2	-3.7		-3.1	G protein-coupled receptor	-	360	818
47	12	membrane protein	34698_at	HG-U95A	M30704	NM_001657	NP_001648	AREG	4q13-q21	-2.3	-4.2	-4.8	-5.2	-14.6		amphiregulin (schwannoma-derived growth factor)	Mol Cell Biol 10:1980-81(1990)	361	819
48	12	membrane protein	38223_at	HG-U95A	AB024037	NM_007063	NP_008994	VRP	2q11.1-q11.2			-2.5		-2	-2.4	vascular Rab-GAP/TBC-containing	Nucleic Acids Res. 27:2391-2400 (1999)	362	820
49	12	membrane protein	38378_at	HG-U95A	X76534	NM_002510	NP_002501	GPNMB	7p15	-3.3		3.9	4.8	-2.2		glycoprotein (transmembrane) nmb	Int. J. Cancer 60:73-81 (1995)	363	821
50	12	membrane protein	38750_at	HG-U95A	U97669	NM_020435	NP_065168	NOTCH3	19p13.2-p13.1	-2.9	-3.5	-4.6	-2.7	-4.3	-3.5	Notch homolog 3	Nat. Genet. 3:256-259 (1993)	364	822
51	12	membrane protein	39310_at	HG-U95A	X86183	NM_000823	NP_000814	BDKRB2	14q32.1-q32.2	-2.1				-2.4	-4.2	bradykinin receptor B2	Biochem. Biophys. Res. Commun. 184:260-268 (1992)	365	823
52	12	membrane protein	40990_at	HG-U95A	AF085389	NM_005723	NP_005714	TSPAN-5	4q23		-2.8	-3.6	-2.8	-3.2	-6	tetraspan 5	Biochim. Biophys. Acta 1399:101-104 (1998)	366	824

Table 23



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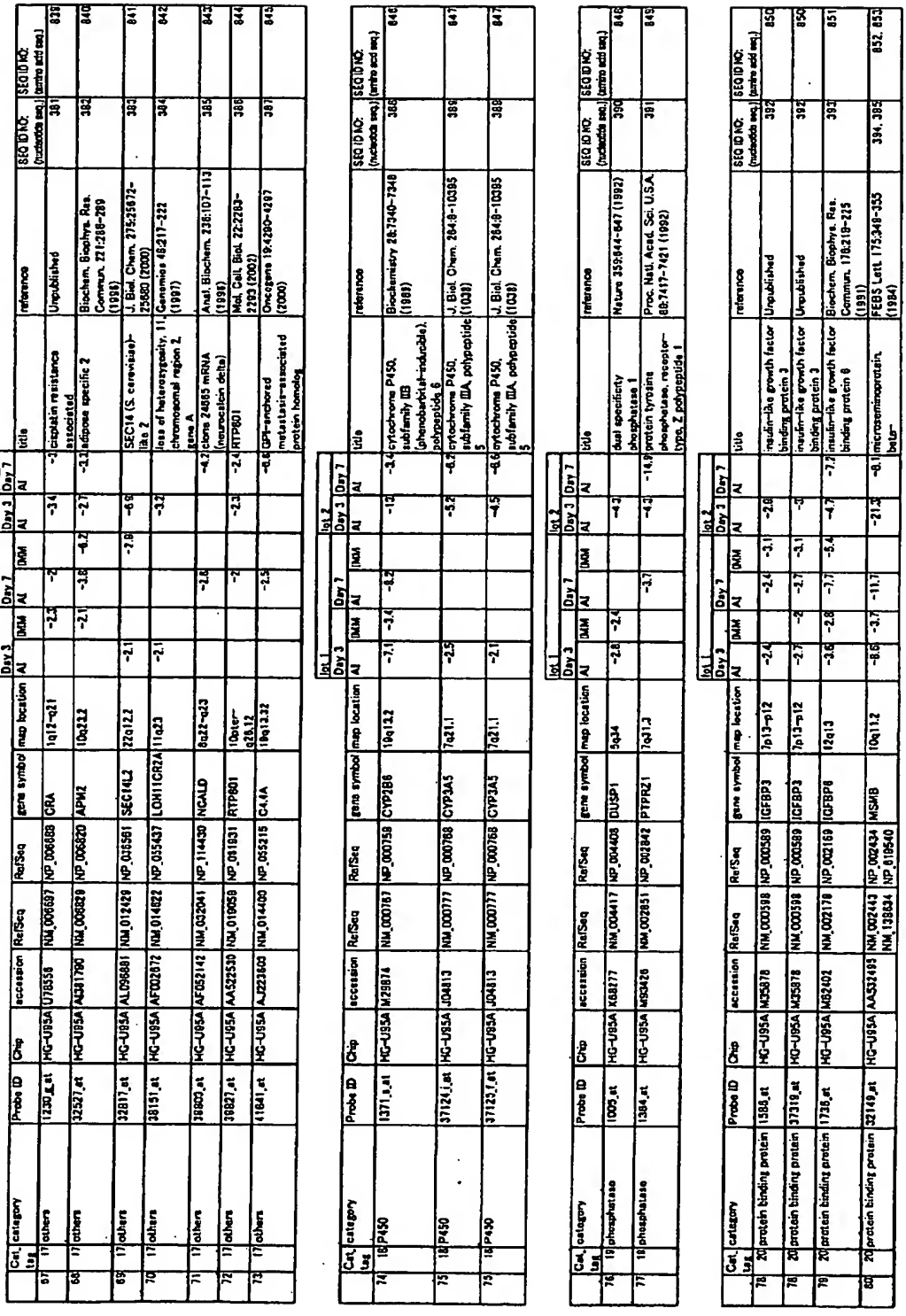
53	13	metabolism	32348_at	HG-U95A	AJ238979	NM_007183	NP_009124	ANXA10	4q33			-2.5		-7.5	-18.9	annexin A10	Cancer Res. 56:3441-3445 (1996)	367	825
54	13	metabolism	32484_at	HG-U95A	AF071216	NM_004942	NP_004933	DEFB2	8p23.1-p22			-4.3			-2.6	defensin, beta 2	Nature 387:- (1997)	368	826
55	13	metabolism	38498_at	HG-U95A	AF014398	NM_014214	NP_055028	INPA2	18p11.2	-2.8		-2			-2.7	inositol(myo)-1(or 4)-monophosphatase 2	Biochem. Biophys. Res. Commun. 251:111-118 (1998)	369	827
56	13	metabolism	37399_at	HG-U95A	D17793	NM_000739	NP_000730	AKR1C3	10p15-p14	-3.5		-4		-2.5	-2.6	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, t	Proc. Natl. Acad. Sci. U.S.A. 80:3183-3187 (1983)	370	828
57	13	metabolism	37482_at	HG-U95A	U37100	NM_020989	NP_066695	AKR1B10	7q33	-6.5	-2.6	-7.5	-6.7	-7.1	-6.7	NM_020299 (analysis) aldo-keto reductase family 1, member B10 (aldose reductase)	J. Biol. Chem. 273 (10):11429-11435 (1998)	371	829
58	13	metabolism	39769_at	HG-U95A	M94856	NM_001444	NP_001435	FABP5	8q21.13			-4.2	-3.7	-3	-3	fatty acid binding protein 5 (psoriasis-associated)	J. Invest. Dermatol. 99:299-305 (1992)	372	830

	Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 3 DMM	lot 1 Day 7 AI	lot 1 Day 7 DMM	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
58	14	MHC	38095_i_at	HG-U95A	M83664	NM_002121	NP_002112	HLA-DPB1	6p21.3			-4.4			-2.5	major histocompatibility complex, class II, DP beta 1	Cell 38:241-249 (1984)	373	831
59	14	MHC	38096_f_at	HG-U95A	M83664	NM_002121	NP_002112	HLA-DPB1	6p21.3			-2.6			-3.3	major histocompatibility complex, class II, DP beta 1	Cell 38:241-249 (1984)	373	831

	Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 3 DMM	lot 1 Day 7 AI	lot 1 Day 7 DMM	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
60	15	MMP related	1008_at	HG-U95A	X07820	NM_002425	NP_002416	MMP10	11q223	-6.3	-3.4			-30.3	-35.2	matrix metalloproteinase 10 preproprotein	Biochem. J. 253:187-192 (1988)	374	832
61	15	MMP related	31859_at	HG-U95A	J05070	NM_004994	NP_004985	MMP9	20q11.2-q13.1	-25.5	-7.3	-10.8	-16	-16	-113.5	matrix metalloproteinase 9 preproprotein	J. Biol. Chem. 264:17213-17221 (1989)	375	833

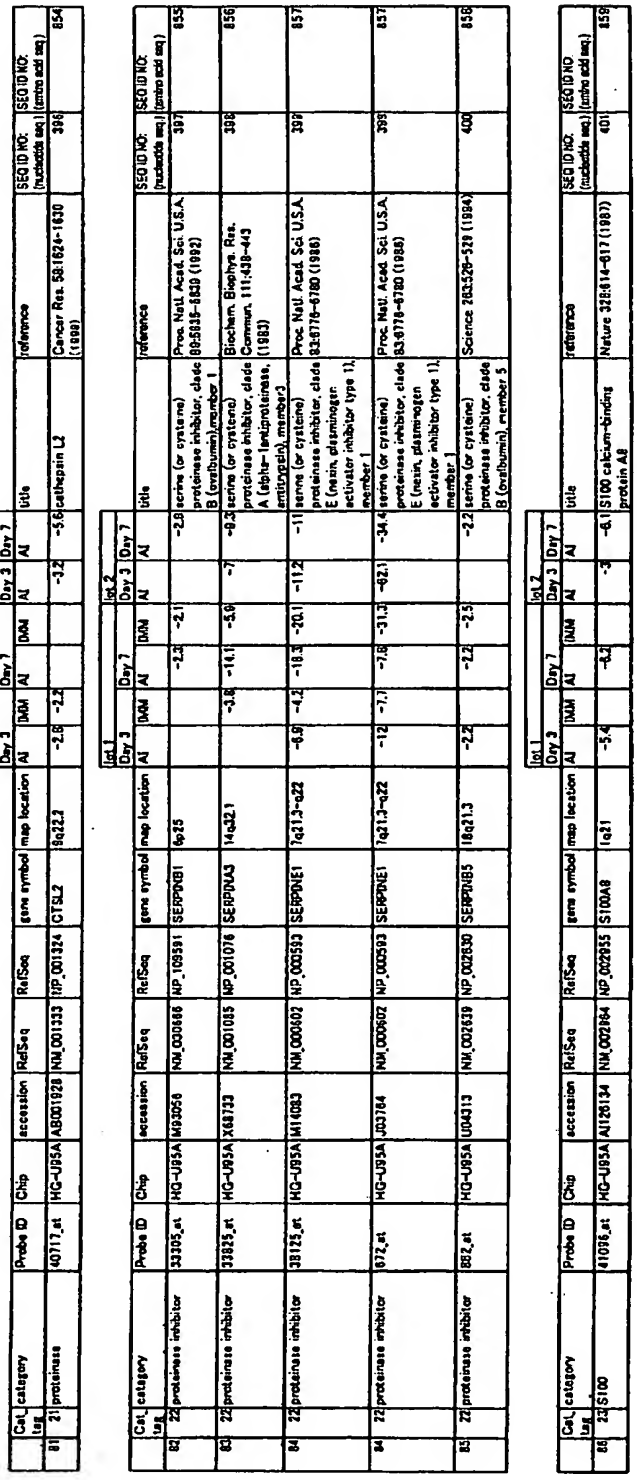
	Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 3 DMM	lot 1 Day 7 AI	lot 1 Day 7 DMM	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
62	16	oncogenesis	1915_s_at	HG-U95A	Y01512	NM_005252	NP_005243	c-fos	14q24.3	-2			-4.3	-2	-2.3	cellular oncogene c-fos (complete sequence)	Proc. Natl. Acad. Sci. U.S.A. 80:3183-3187 (1983)	376	834
63	16	oncogenesis	1916_s_at	HG-U95A	Y01512	NM_005252	NP_005243	c-fos	14q24.3	-2.2		-2.6	-4.7	-3.1	-3.6	cellular oncogene c-fos (complete sequence)	Proc. Natl. Acad. Sci. U.S.A. 80:3183-3187 (1983)	376	834
64	16	oncogenesis	36933_at	HG-U95A	D87953	NM_006096	NP_006087	NDRG1	8q24	-4.8	-2.3	-3.6	-2.4	-2.8		N-myc downstream regulated gene 1	J. Biol. Chem. 271:9-28685 (2965)	377	835
65	16	oncogenesis	37283_at	HG-U95A	X82209	NM_002430	NP_002421	MN1	22q12.1			-3.2			-7.3	meningioma 1	Oncogene 10:1521-1528 (1995)	378	836
66	16	oncogenesis	37821_at	HG-U95A	AF041260	NM_003857	NP_003848	BCAS1	20q13.2-q13.3			-3.7		-4.8	-13.2	breast carcinoma amplified sequence 1	Cancer Res. 56:3441-3445 (1996)	379	837
67	16	oncogenesis	38827_at	HG-U95A	AF038451	NM_006408	NP_006399	AGR2	7p21.3			-2.7			-3.7	anterior gradient 2 homolog (Xenopus laevis)	Biochem. Biophys. Res. Commun. 251:111-118 (1998)	380	838

Table 24



Cat. tag	category	Probe ID	Chip	accession	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 3 DMM	lot 1 Day 7 AI	lot 1 Day 7 DMM	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
67	17	others	1230_g_at	HG-U95A	U76638	NM_006687	NP_006688	CRA	1q12-q21		-2.5	-2	-3.4	-3	cisplatin resistance associated	Unpublished	381	839
68	17	others	32527_at	HG-U95A	AB31790	NM_006820	NP_006820	APM2	10q23.2		-2.1	-1.8	-4.2	-2.7	adipose specific 2	Biochem. Biophys. Res. Commun. 221:286-289 (1996)	382	840
69	17	others	32817_at	HG-U95A	AL096881	NM_012429	NP_036561	SEC14L2	22q12.2		-2.1		-2.8	-6.9	SEC14 (S. cerevisiae)-like 2	J. Biol. Chem. 275:25672-25680 (2000)	383	841
70	17	others	38151_at	HG-U95A	AF002672	NM_014822	NP_055437	LOH11CR2A	11q23		-2.1			-3.2	loss of heterozygosity, 11, chromosomal region 2, gene A	Genomics 48:211-222 (1997)	384	842
71	17	others	38800_at	HG-U95A	AF052142	NM_032041	NP_114439	NCALD	8q22-q23			-2.6		-4.2	clone 24665 mRNA (neurocalcin delta)	Anat. Biochem. 236:107-113 (1996)	385	843
72	17	others	38827_at	HG-U95A	AA532530	NM_019058	NP_061931	RTP801	10cter-q26.12			-2		-2.4	RTP801	Mol. Cell. Biol. 22:2283-2293 (2002)	386	844
73	17	others	41841_at	HG-U95A	AJ223603	NM_014400	NP_055215	C4.4A	19q13.32			-2.5		-6.8	GPI-anchored metastasis-associated protein homolog	Oncogene 19:4280-4287 (2000)	387	845
74	18	P450	1371_s_at	HG-U95A	M29874	NM_000767	NP_000758	CYP2B6	19q13.2		-7.1	-3.4	-8.2	-10	cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6	Biochemistry 28:7340-7348 (1989)	388	846
75	18	P450	37124_i_at	HG-U95A	J04813	NM_000777	NP_000768	CYP3A5	7q21.1		-2.5			-5.2	cytochrome P450, subfamily IIIA, polypeptide 5	J. Biol. Chem. 264:8-10385 (1038)	389	847
75	18	P450	37123_f_at	HG-U95A	J04813	NM_000777	NP_000768	CYP3A5	7q21.1		-2.1			-4.5	cytochrome P450, subfamily IIIA, polypeptide 5	J. Biol. Chem. 264:8-10385 (1038)	388	847
76	19	phosphatase	1005_at	HG-U95A	X68277	NM_004417	NP_004408	DUSP1	5q34		-2.8	-2.4		-4.2	dual specificity phosphatase 1	Nature 359:844-847 (1992)	390	848
77	19	phosphatase	1384_at	HG-U95A	M92426	NM_002851	NP_002842	PTPR21	7q31.3			-3.7		-14.9	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	Proc. Natl. Acad. Sci. U.S.A. 89:7417-7421 (1992)	391	849
78	20	protein binding protein	1588_at	HG-U95A	M35878	NM_000598	NP_000589	IGFBP3	7p13-p12		-2.4		-2.4	-3.1	-2.8	insulin-like growth factor binding protein 3	Unpublished	392	850
78	20	protein binding protein	37319_at	HG-U95A	M35878	NM_000598	NP_000589	IGFBP3	7p13-p12		-2.7	-2	-2.7	-3.1	-3	insulin-like growth factor binding protein 3	Unpublished	392	850
79	20	protein binding protein	1736_at	HG-U95A	M62402	NM_002178	NP_002169	IGFBP6	12q13		-3.6	-2.8	-7.7	-5.4	-4.7	insulin-like growth factor binding protein 6	Biochem. Biophys. Res. Commun. 178:218-225 (1991)	393	851
80	20	protein binding protein	32149_at	HG-U95A	AA532495	NM_002443 NM_138834	NP_002434 NP_619540	MSMB	10q11.2		-8.6	-3.7	-11.7		-21.2	-8.1	microseminoprotein, beta-	FEBS Lett. 175:349-355 (1984)	394, 395	852, 853

Table 25



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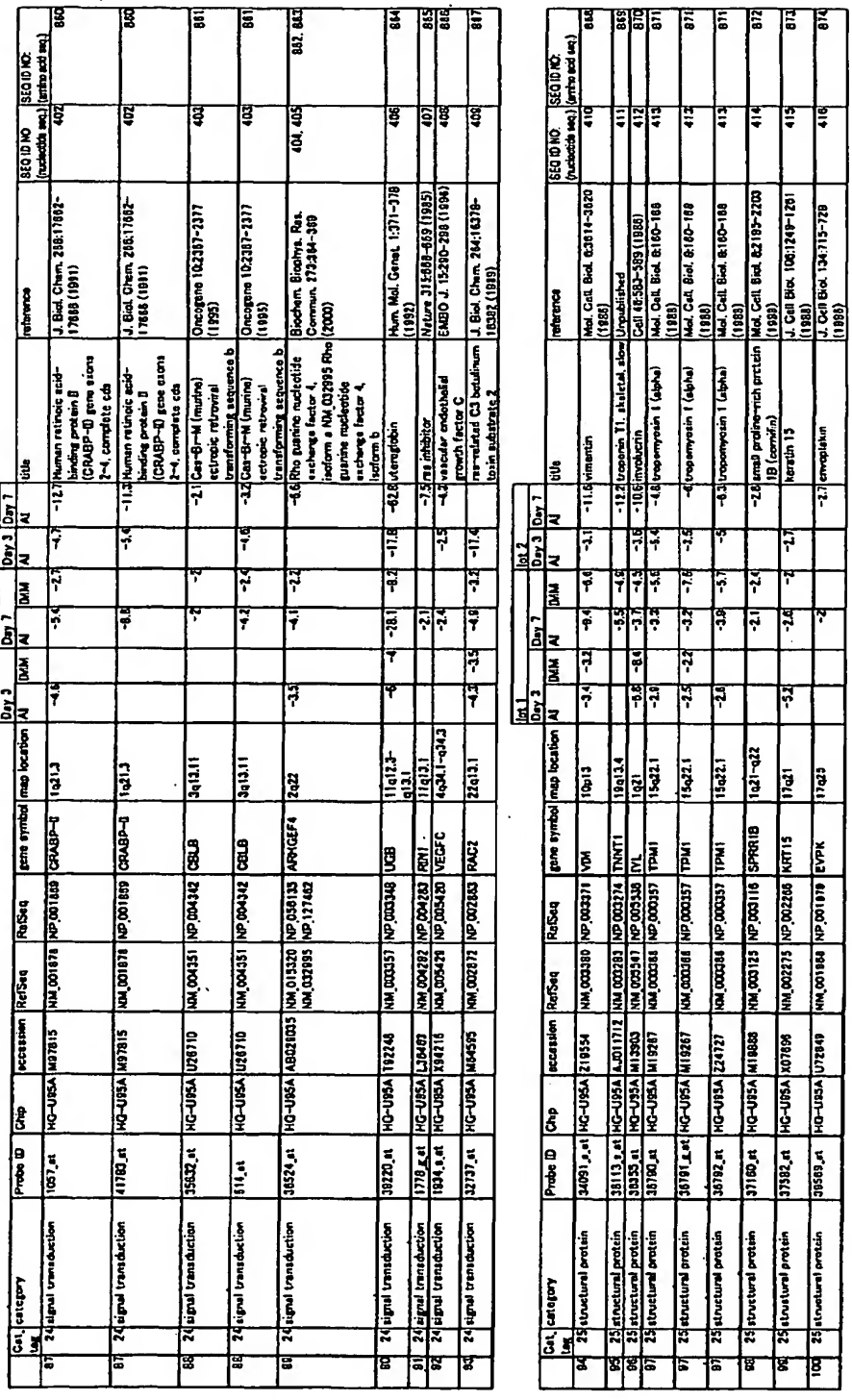
81	21	proteinase	40717_at	HG-U95A	AB001928	NM_001333	NP_001324	CTSL2	9q22.2	-2.8	-2.2			-3.2	-5.6	cathepsin L2	Cancer Res. 58:1624-1630 (1998)	396	854

	Cat_tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lgt 1 Day 3 AI	lgt 1 Day 3 DMM	lgt 1 Day 7 AI	lgt 1 Day 7 DMM	lgt 2 Day 3 AI	lgt 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
82	22	proteinase inhibitor	33305_at	HG-U95A	M93056	NM_000488	NP_109591	SERPINB1	6p25			-2.2	-2.1		-2.8	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1	Proc. Natl. Acad. Sci. U.S.A. 89:5535-5539 (1992)	397	855
83	22	proteinase inhibitor	33825_at	HG-U95A	X68733	NM_001085	NP_001076	SERPINA3	14q32.1		-3.6	-14.1	-5.9	-7	-9.3	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	Biochem. Biophys. Res. Commun. 111:439-445 (1983)	398	856
84	22	proteinase inhibitor	38128_at	HG-U95A	M14083	NM_000602	NP_000593	SERPINE1	7q21.3-q22	-6.9	-4.2	-18.3	-20.1	-11.2	-11	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	Proc. Natl. Acad. Sci. U.S.A. 83:8778-8780 (1986)	399	857
84	22	proteinase inhibitor	672_at	HG-U95A	J03764	NM_000602	NP_000593	SERPINE1	7q21.3-q22	-12	-7.7	-7.6	-31.1	-62.1	-34.4	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	Proc. Natl. Acad. Sci. U.S.A. 83:8778-8780 (1986)	399	857
85	22	proteinase inhibitor	882_at	HG-U95A	U04313	NM_002639	NP_002630	SERPINB5	18q21.3	-2.2		-2.2	-2.5		-2.2	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5	Science 263:526-529 (1994)	400	858

	Cat_tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lgt 1 Day 3 AI	lgt 1 Day 3 DMM	lgt 1 Day 7 AI	lgt 1 Day 7 DMM	lgt 2 Day 3 AI	lgt 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
86	23	S100	41096_at	HG-U95A	AI126134	NM_002964	NP_002955	S100A8	1q21	-5.4		-8.2		-3	-6.1	S100 calcium-binding protein A8	Nature 328:814-817 (1987)	401	859

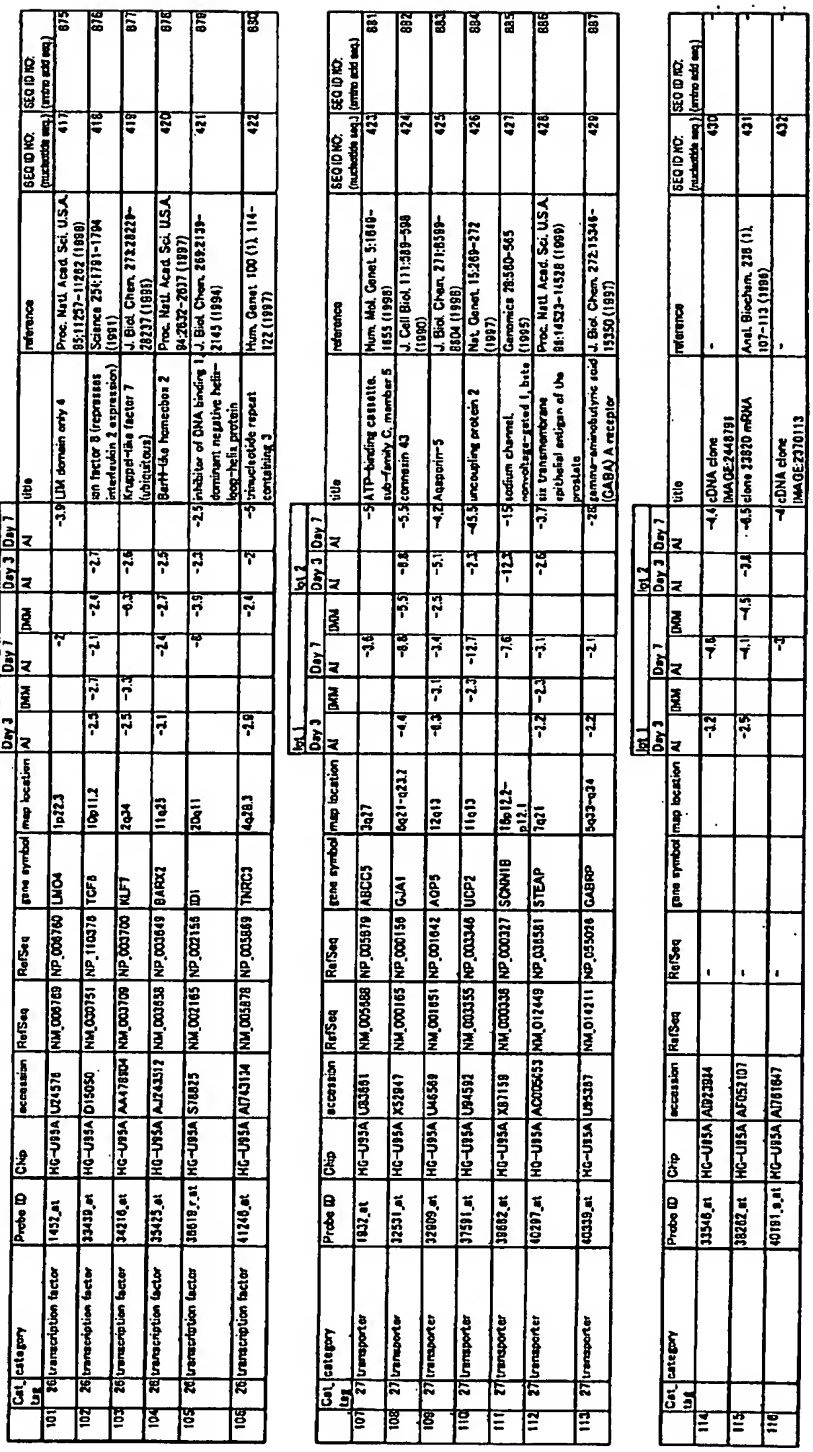
Table 26



	Cat. No.	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 3 DMM	lot 1 Day 7 AI	lot 1 Day 7 DMM	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
87	24	signal transduction	1057_at	HG-U95A	M97815	NM_001878	NP_001869	CRABP-II	1q21.3	-4.6		-5.4	-2.7	-4.7	-12.7	Human retinoic acid-binding protein II (CRABP-II) gene exons 2-4, complete cds	J. Biol. Chem. 268:17862-17868 (1991)	402	860
87	24	signal transduction	41783_at	HG-U95A	M97815	NM_001878	NP_001869	CRABP-II	1q21.3			-8.8		-5.4	-11.3	Human retinoic acid-binding protein II (CRABP-II) gene exons 2-4, complete cds	J. Biol. Chem. 268:17862-17868 (1991)	402	860
88	24	signal transduction	35632_at	HG-U95A	U26710	NM_004351	NP_004342	CBLB	3q13.11			-2	-2		-2.1	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	Oncogene 10:2367-2377 (1995)	403	861
88	24	signal transduction	514_at	HG-U95A	U26710	NM_004351	NP_004342	CBLB	3q13.11			-4.2	-2.4	-4.6	-3.2	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	Oncogene 10:2367-2377 (1995)	403	861
90	24	signal transduction	38524_at	HG-U95A	AB021035	NM_015320 NM_032995	NP_056133 NP_127462	ARHGEF4	2q22	-3.5		-4.1	-2.2		-6.6	Rho guanine nucleotide exchange factor 4, isoform a NM_032995 Rho guanine nucleotide exchange factor 4, isoform b	Biochem. Biophys. Res. Commun. 273:384-389 (2000)	404, 405	862, 863
90	24	signal transduction	38220_at	HG-U95A	19224B	NM_000357	NP_000348	UCB	11q12.3-q13.1	-6	-4	-28.1	-8.2	-11.8	-62.8	dermatopontin	Hum. Mol. Genet. 1:371-378 (1992)	406	864
91	24	signal transduction	1778_g_at	HG-U95A	L38487	NM_004282	NP_004263	RIN1	11q13.1			-2.1			-7.5	ras inhibitor	Nature 314:686-689 (1985)	407	865
92	24	signal transduction	1934_s_at	HG-U95A	X94715	NM_005428	NP_005420	VEGFC	4q34.1-q34.3			-2.4		-2.5	-4.3	vascular endothelial growth factor C	EMBO J. 15:290-298 (1994)	408	866
93	24	signal transduction	32737_at	HG-U95A	M64595	NM_002872	NP_002863	RAC2	22q13.1	-4.3	-3.5	-4.8	-3.2	-11.4		ras-related C3 botulinum toxin substrate 2	J. Biol. Chem. 264:16378-16382 (1989)	409	867

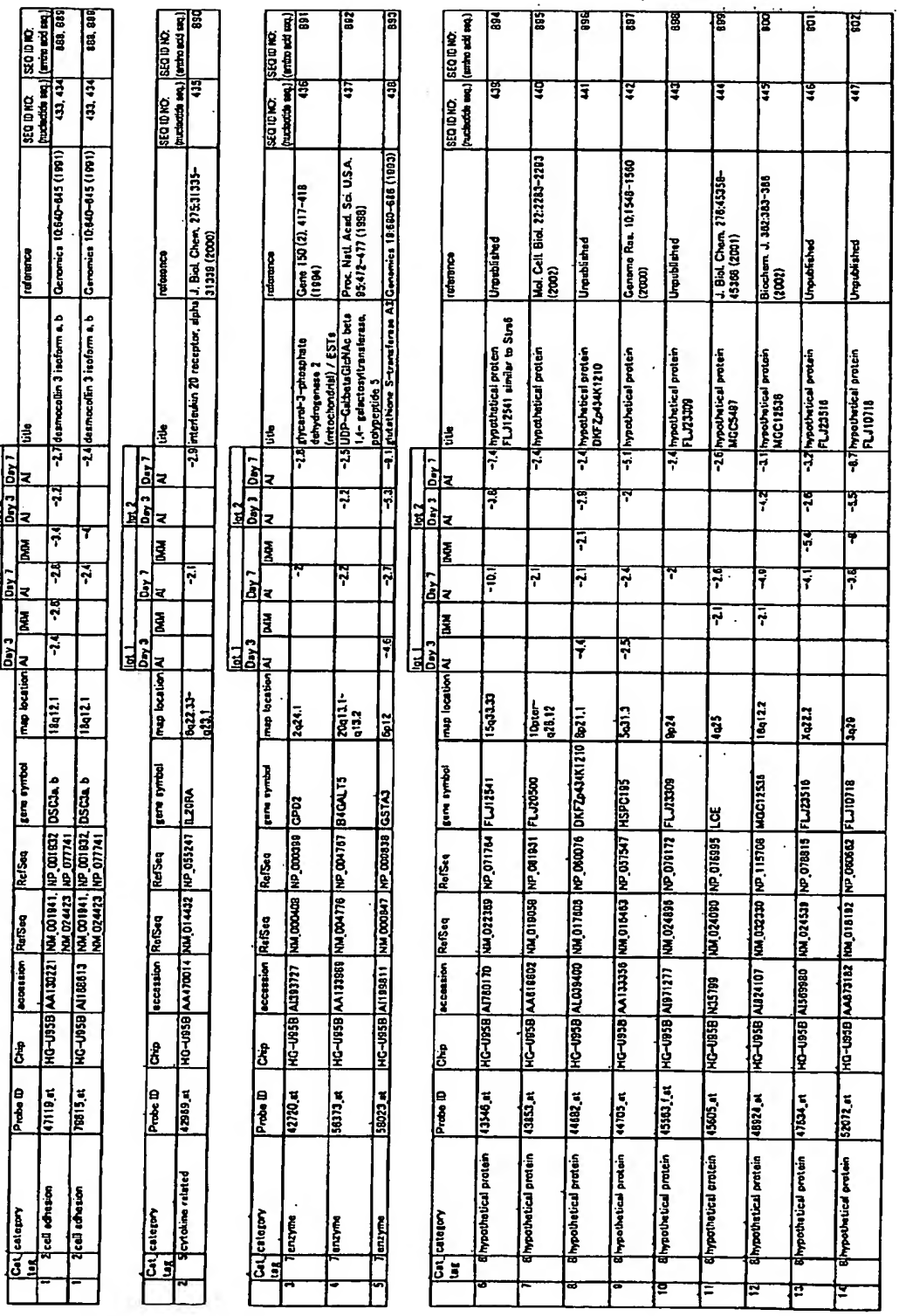
	Cat. No.	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 3 DMM	lot 1 Day 7 AI	lot 1 Day 7 DMM	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
94	25	structural protein	34091_g_at	HG-U95A	21554	NM_003380	NP_003371	VIM	10p13	-3.4	-3.2	-9.4	-6.6	-3.1	-11.8	vimentin	Mol. Cell. Biol. 6:3614-3620 (1986)	410	868
95	25	structural protein	38113_s_at	HG-U95A	AJ011712	NM_003283	NP_003274	TNNT1	19q13.4			-5.5	-4.6		-12.7	troponin T1, skeletal, slow	Unpublished	411	869
96	25	structural protein	38135_at	HG-U95A	M13903	NM_003547	NP_003538	IVL	1q21	-6.8	-6.4	-9.7	-4.9	-3.6	-10.6	involucrin	Cell 46:583-589 (1986)	412	870
97	25	structural protein	38780_at	HG-U95A	M19267	NM_000358	NP_000357	TPM1	15q22.1	-2.8		-3.8	-5.6	-5.4	-4.8	tropomyosin 1 (alpha)	Mol. Cell. Biol. 8:160-166 (1988)	413	871
97	25	structural protein	38781_g_at	HG-U95A	M19267	NM_000358	NP_000357	TPM1	15q22.1	-2.5	-2.2	-3.2	-2.6	-3.5	-4	tropomyosin 1 (alpha)	Mol. Cell. Biol. 8:160-166 (1988)	412	871
97	25	structural protein	38782_at	HG-U95A	Z24727	NM_000358	NP_000357	TPM1	15q22.1	-2.8		-3.9	-5.7	-5	-6.3	tropomyosin 1 (alpha)	Mol. Cell. Biol. 8:160-166 (1988)	413	871
98	25	structural protein	37160_at	HG-U95A	M18888	NM_003123	NP_003116	SPR91B	1q21-q22			-2.1	-2.4		-2.8	small proline-rich protein 1B (cornifin)	Mol. Cell. Biol. 8:2195-2200 (1988)	414	872
99	25	structural protein	37582_at	HG-U95A	X07696	NM_002275	NP_002266	KRT15	17q21	-5.2	-2.6	-2.6	-2	-2.7		keratin 15	J. Cell Biol. 106:1249-1261 (1988)	415	873
100	25	structural protein	39569_at	HG-U95A	U72649	NM_001958	NP_001979	EVPK	17q25			-2			-2.1	envoplakin	J. Cell Biol. 134:715-729 (1996)	416	874

Table 27



	Cat_tgt	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lot 1 Day 3 AI	lot 1 Day 7 DMM	lot 1 Day 7 AI	lot 2 Day 3 AI	lot 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
101	26	transcription factor	1452_at	HG-U95A	U24578	NM_006760	NP_006760	LMO4	1p22.3		-2			-3.9	LIM domain only 4	Proc. Natl. Acad. Sci. U.S.A. 95:11257-11262 (1998)	417	875
102	26	transcription factor	33419_at	HG-U95A	D15050	NM_003751	NP_116378	TCF8	10p11.2	-2.5	-2.7	-2.1	-2.4	-2.7	zinc finger E-box binding homeobox 1	Science 254:1781-1784 (1991)	418	876
103	26	transcription factor	34218_at	HG-U95A	AA178804	NM_003709	NP_003700	KLF7	2p24	-2.5	-3.3		-6.3	-2.6	interleukin 2 expression) Kruppel-like factor 7 (ubiquitous)	J. Biol. Chem. 273:28229-28237 (1998)	419	877
104	26	transcription factor	35423_at	HG-U95A	AJ243312	NM_003838	NP_003829	BARX2	11q25	-2.1		-2.4	-2.7	-2.5	BarH-like homeobox 2	Proc. Natl. Acad. Sci. U.S.A. 94:2632-2637 (1997)	420	878
105	26	transcription factor	38619_r_at	HG-U95A	S78825	NM_002165	NP_002155	ID1	20q11		-6	-3.9	-2.3	-2.5	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	J. Biol. Chem. 269:2139-2145 (1994)	421	879
106	26	transcription factor	41240_at	HG-U95A	AI743134	NM_005878	NP_005869	TNRC3	4q28.3	-2.9		-2.4	-2	-5	trinucleotide repeat containing 3	Hum. Genet. 100 (1), 114-122 (1997)	422	880
107	27	transporter	1832_at	HG-U95A	U83861	NM_005688	NP_005679	ABCC5	3q27		-3.6			-5	ATP-binding cassette, sub-family C, member 5	Hum. Mol. Genet. 5:1849-1855 (1996)	423	881
108	27	transporter	32531_at	HG-U95A	X52947	NM_000165	NP_000156	GJA1	6q21-q23.2	-4.4	-8.8	-5.5	-0.8	-5.5	connexin 43	J. Cell Biol. 111:589-598 (1990)	424	882
109	27	transporter	32609_at	HG-U95A	U46569	NM_001651	NP_001642	AQP5	12q13	-4.3	-3.1	-3.4	-2.5	-5.1	Aquaporin-5	J. Biol. Chem. 271:8599-8604 (1996)	425	883
110	27	transporter	37591_at	HG-U95A	U84592	NM_003355	NP_003335	UCP2	11q13		-2.3	-12.7	-2.3	-45.5	uncoupling protein 2	Nat. Genet. 15:269-272 (1997)	426	884
111	27	transporter	38682_at	HG-U95A	X87159	NM_000338	NP_000327	SCN4B	11q13.2-q13.1		-7.6	-12.3	-1.5	-15	sodium channel, nonvoltage-gated 1 beta	Genomics 28:560-565 (1995)	427	885
112	27	transporter	40297_at	HG-U95A	AC005633	NM_012449	NP_036581	STEAP	7q21	-2.2	-2.3	-3.1		-3.7	six transmembrane epithelial antigen of the prostate	Proc. Natl. Acad. Sci. U.S.A. 96:14523-14528 (1999)	428	886
113	27	transporter	40339_at	HG-U95A	U95367	NM_014211	NP_055026	GABRP	5q33-q34	-2.2	-2.1			-25	gamma-aminobutyric acid (GABA) A receptor	J. Biol. Chem. 272:15346-15350 (1997)	429	887
114			33548_at	HG-U95A	AI023804		-							-4.4	cDNA clone IMAGE:2448191	-	430	-
115			33582_at	HG-U95A	AF052107		-							-3.8	clone 23920 mRNA	Anal. Biochem. 238 (1), 107-113 (1996)	431	-
116			40191_s_at	HG-U95A	AI761647		-							-4	cDNA clone IMAGE:2370113	-	432	-

Table 28



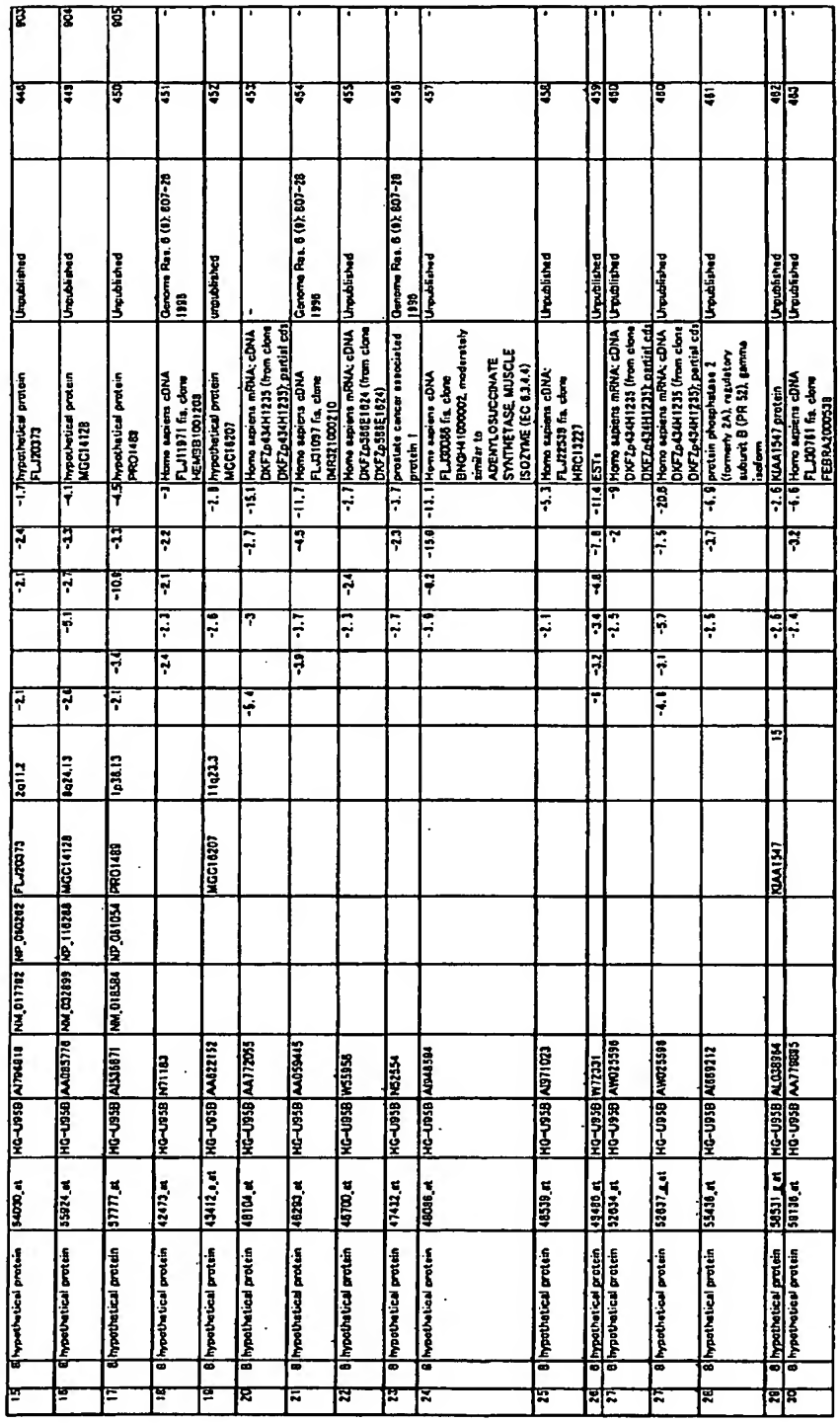
Cat tag	category	Probe ID	Chip	accession	RefSeq	gene symbol	map location	lgt 1 Day 3 AI	lgt 1 Day 3 DMM	lgt 1 Day 7 AI	lgt 1 Day 7 DMM	lgt 2 Day 3 AI	lgt 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
1	2 cell adhesion	47119_at	HG-U95B	AA130221	NM_001841, NP_001832 NM_024423 NP_077741	DSC3a, b	18q12.1	-2.4	-2.6	-2.6	-3.4	-2.2	-2.7	desmocollin 3 isoform a, b	Genomics 10:640–645 (1991)	433, 434	888, 889
1	2 cell adhesion	78815_at	HG-U95B	AI188613	NM_001841, NP_001832 NM_024423 NP_077741	DSC3a, b	18q12.1			-2.4	-4		-2.4	desmocollin 3 isoform a, b	Genomics 10:640–645 (1991)	433, 434	888, 889

Cat tag	category	Probe ID	Chip	accession	RefSeq	gene symbol	map location	lgt 1 Day 3 AI	lgt 1 Day 3 DMM	lgt 1 Day 7 AI	lgt 1 Day 7 DMM	lgt 2 Day 3 AI	lgt 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
2	3 cytokine related	42989_at	HG-U95B	AA470014	NM_014432	NP_055247	IL20RA	9q22.33-q23.1			-2.1		-2.9	interleukin 20 receptor, alpha	J. Biol. Chem. 275:31335–31339 (2000)	435	890

Cat tag	category	Probe ID	Chip	accession	RefSeq	gene symbol	map location	lgt 1 Day 3 AI	lgt 1 Day 3 DMM	lgt 1 Day 7 AI	lgt 1 Day 7 DMM	lgt 2 Day 3 AI	lgt 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
3	7 enzyme	42750_at	HG-U95B	AI393727	NM_000408	GPD2	2q24.1			-2			-2.8	glycerol-3-phosphate dehydrogenase 2 (mitochondrial) / EST6	Gene 150(2), 417–418 (1994)	436	891
4	7 enzyme	56373_at	HG-U95B	AA133868	NM_004776	B4GALT5	20q13.1-q13.2			-2.2		-2.2	-2.5	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	Proc. Natl. Acad. Sci. U.S.A. 95:472–477 (1998)	437	892
5	7 enzyme	59023_at	HG-U95B	AI199811	NM_000847	GSTA3	6p12	-4.6		-2.7		-5.3	-4.1	glutathione S-transferase A3	Genomics 19:680–686 (1993)	438	893

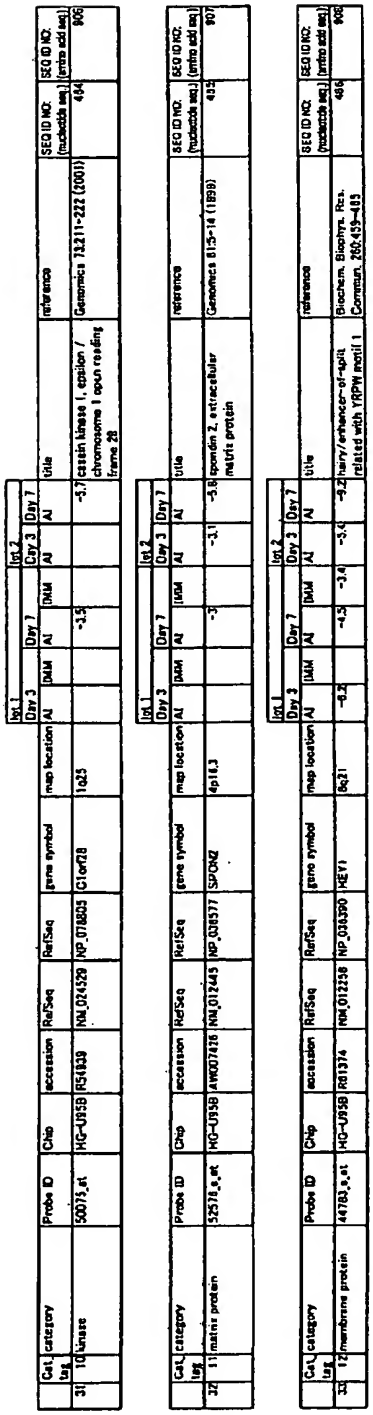
Cat tag	category	Probe ID	Chip	accession	RefSeq	gene symbol	map location	lgt 1 Day 3 AI	lgt 1 Day 3 DMM	lgt 1 Day 7 AI	lgt 1 Day 7 DMM	lgt 2 Day 3 AI	lgt 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
6	8 hypothetical protein	43546_at	HG-U95B	AI760170	NM_022389	NP_071764	FLJ12541	15q33.33		-10.1		-3.8	-7.4	hypothetical protein FLJ12541 similar to Sin6	Unpublished	439	894
7	8 hypothetical protein	43853_at	HG-U95B	AA618602	NM_018058	NP_060528	FLJ20500	10pter-q26.12		-2.1			-2.4	hypothetical protein	Mol. Cell Biol. 22:2283–2293 (2002)	440	895
8	8 hypothetical protein	44682_at	HG-U95B	AL039409	NM_017608	NP_060076	DKFZp434K1210	8p21.1	-4.6	-2.1	-2.1	-1.8	-2.4	hypothetical protein DKFZp434K1210	Unpublished	441	896
9	8 hypothetical protein	44703_at	HG-U95B	AA133356	NM_016463	NP_057547	HSPC105	5q31.3	-2.5	-2.4		-2	-5.1	hypothetical protein	Genome Res. 10:1548–1560 (2000)	442	897
10	8 hypothetical protein	45363_at	HG-U95B	AI971277	NM_024898	NP_079172	FLJ23309	9p24		-2			-2.4	hypothetical protein FLJ23309	Unpublished	443	898
11	8 hypothetical protein	45605_at	HG-U95B	N35799	NM_024090	NP_076995	LOC	4q25	-2.1	-2.6			-2.6	hypothetical protein MGC5487	J. Biol. Chem. 276:45358–45366 (2001)	444	899
12	8 hypothetical protein	46924_at	HG-U95B	AI824107	NM_032330	NP_115708	MGC11538	16q12.2	-2.1	-4.0		-4.2	-3.1	hypothetical protein MGC11538	Biochem. J. 362:363–369 (2002)	445	900
13	8 hypothetical protein	47834_at	HG-U95B	AI569980	NM_024539	NP_078815	FLJ23516	Xq12.2		-4.1	-5.4	-1.6	-3.2	hypothetical protein FLJ23516	Unpublished	446	901
14	8 hypothetical protein	52072_at	HG-U95B	AA873182	NM_018192	NP_060662	FLJ10718	3q29		-3.6	-6	-5.5	-6.7	hypothetical protein FLJ10718	Unpublished	447	902

Table 29



15	0	hypothetical protein	54030_at	HG-U95B	AI764818	NM_017782	NP_060282	FLJ20073	2q11.2	-2.1			-2.1	-2.4	-1.7	hypothetical protein FLJ20073	Unpublished		448	903
16	0	hypothetical protein	55924_at	HG-U95B	AA085778	NM_032699	NP_116088	MGC14128	8q24.13	-2.4		-5.1	-2.7	-3.3	-4.1	hypothetical protein MGC14128	Unpublished		449	904
17	0	hypothetical protein	57777_at	HG-U95B	AI338871	NM_018584	NP_061054	PRO1488	1p36.13	-2.1	-3.4		-10.8	-3.3	-4.5	hypothetical protein PRO1488	Unpublished		450	905
18	0	hypothetical protein	42473_at	HG-U95B	W71183					-2.4	-2.3	-2.1	-2.2	-3		Homo sapiens cDNA FLJ11971 fis, clone HEMBB1001268	Genome Res. 6 (9): 807-28 1996		451	-
19	0	hypothetical protein	43412_s_at	HG-U95B	AA422152			MGC18207	11q23.3			-2.6				hypothetical protein MGC18207	unpublished		452	-
20	0	hypothetical protein	48104_at	HG-U95B	AA772055					-6.4		-3		-1.7	-15.1	Homo sapiens mRNA; cDNA DKFZp434H1235 (from clone DKFZp434H1235); partial cds	-		453	-
21	0	hypothetical protein	48293_at	HG-U95B	AA059445							-3.9	-1.7		-11.7	Homo sapiens cDNA FLJ31097 fis, clone NT2RI2003210	Genome Res. 6 (9): 807-28 1996		454	-
22	0	hypothetical protein	48700_at	HG-U95B	W53958							-2.3	-2.4		-2.7	Homo sapiens mRNA; cDNA DKFZp566E1624 (from clone DKFZp566E1624)	Unpublished		455	-
23	0	hypothetical protein	47442_at	HG-U95B	H52454							-2.7		-2.3	-2.7	prostate cancer associated protein 1	Genome Res. 6 (9): 807-28 1996		456	-
24	0	hypothetical protein	48086_at	HG-U95B	AI344594							-3.6	-4.2	-19.6	-11.1	Homo sapiens cDNA FLJ30088 fis, clone BNGH41000002, moderately similar to ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (EC 6.3.4.4)	Unpublished		457	-
25	0	hypothetical protein	48539_at	HG-U95B	AI371023							-2.1			-3.3	Homo sapiens cDNA: FLJ22539 fis, clone HRC11227	Unpublished		458	-
26	0	hypothetical protein	49486_at	HG-U95B	W72351							-1	-3.2	-4.8	-1.8	-11.4	EST:	Unpublished		459	-
27	0	hypothetical protein	32634_at	HG-U95B	AW023596								-2.5		-2	-9	Homo sapiens mRNA; cDNA DKFZp434H1235 (from clone DKFZp434H1235); partial cds	Unpublished		460	-
28	0	hypothetical protein	52837_s_at	HG-U95B	AW025598							-4.1	-3.1	-5.7	-1.5	-20.5	Homo sapiens mRNA; cDNA DKFZp434H1235 (from clone DKFZp434H1235); partial cds	Unpublished		460	-
29	0	hypothetical protein	53436_at	HG-U95B	AI689312									-1.5	-2.7	-4.9	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform	Unpublished		461	-
30	0	hypothetical protein	58531_s_at	HG-U95B	AL033934			KIAA1347		13		-2.6			-2.6	KIAA1347 protein	Unpublished		462	-
31	0	hypothetical protein	58130_at	HG-U95B	AA778895							-2.4		-3.2	-6.6	Homo sapiens cDNA FLJ30711 fis, clone FEBRA3000538	Unpublished		463	-

Table 30

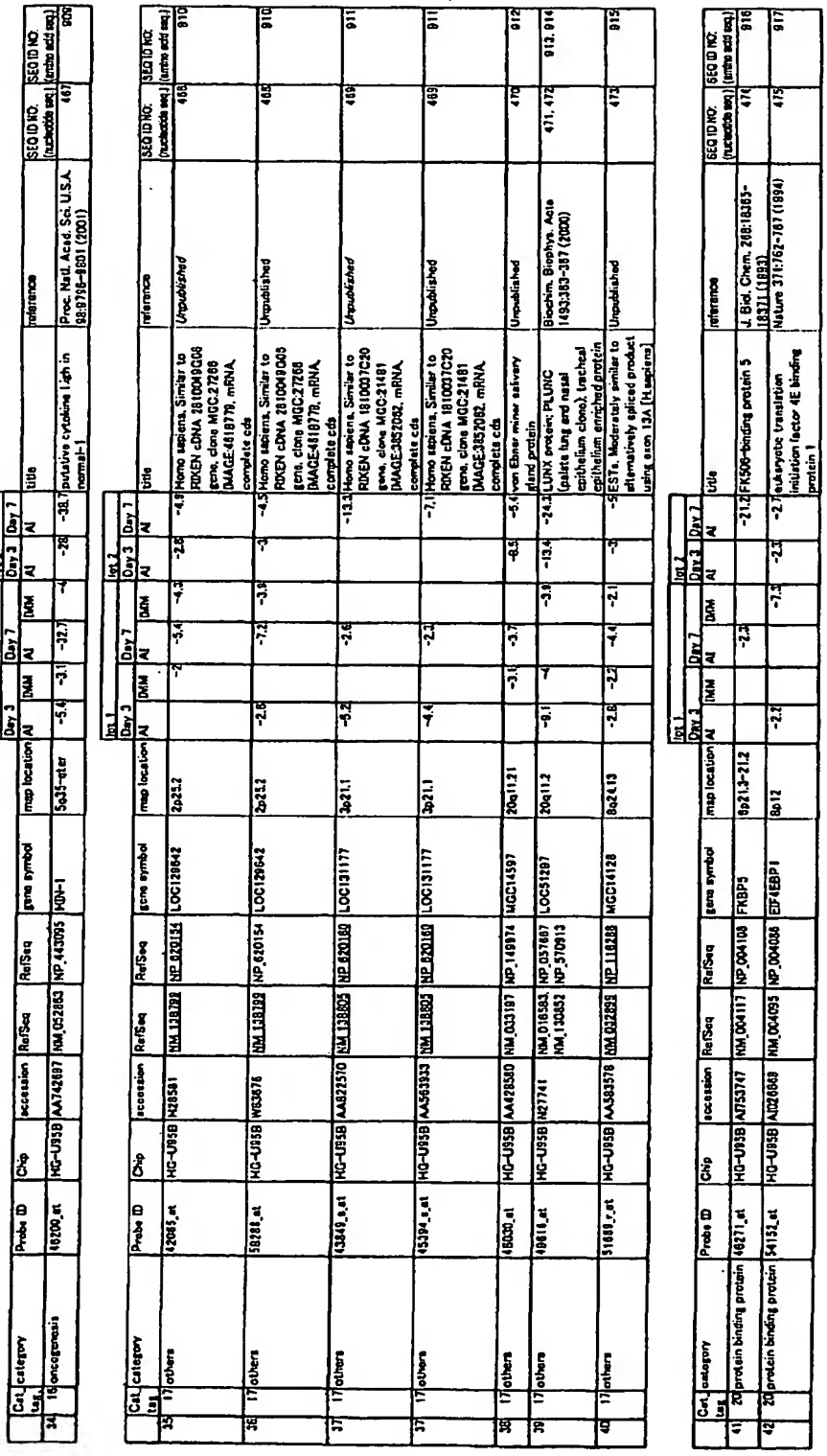


	Cat1 tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Int 1 Day 3 AI	Int 1 Day 3 IMM	Int 1 Day 7 AI	Int 1 Day 7 IMM	Int 2 Day 3 AI	Int 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
31	10	kinase	50075_at	HG-U95B	R54839	NM_024529	NP_078805	C1orf18	1q25			-3.5			-5.7	casein kinase I, epsilon / chromosome 1 open reading frame 28	Genomics 73:211-222 (2001)	484	906

	Cat1 tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Int 1 Day 3 AI	Int 1 Day 3 IMM	Int 1 Day 7 AI	Int 1 Day 7 IMM	Int 2 Day 3 AI	Int 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
32	11	matrix protein	52578_s_at	HG-U95B	AW007428	NM_012445	NP_036577	SPON2	4p16.3			-3		-3.1	-5.8	spondin 2, extracellular matrix protein	Genomics 81:5-14 (1999)	485	907

	Cat1 tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Int 1 Day 3 AI	Int 1 Day 3 IMM	Int 1 Day 7 AI	Int 1 Day 7 IMM	Int 2 Day 3 AI	Int 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
33	12	membrane protein	44783_s_at	HG-U95B	R61374	NM_012258	NP_036390	HEY1	8q21		-8.2		-4.5	-3.4	-9.2	hairy/enhancer-of-split related with YRPW motif 1	Biochem. Biophys. Res. Commun. 260:459-465	486	908

Table 31



Cat. No.	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Int 1 Day 3 AI	Int 1 Day 7 DMM	Int 1 Day 7 AI	Int 2 Day 3 AI	Int 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
34	16 oncogenesis	16209_at	HG-U95B	AA742697	NM_052863	NP_443095	HGH-1	5q33-qter	-5.6	-3.1	-32.7	-4	-28	putative cytokine 1 gh in normal-1	Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801 (2001)	467	909
35	17 others	42085_at	HG-U95B	H28581	NM_138781	NP_620134	LOC129642	2q33.2		-2	-5.4	-4.3	-2.5	-4.9 Homo sapiens, Similar to RIKEN cDNA 2810049G06 gene, clone MGC:27268 IMAGE:4818778, mRNA, complete cds	Unpublished	468	910
36	17 others	58281_at	HG-U95B	W63676	NM_138781	NP_620134	LOC129642	2q33.2	-2.8		-7.2	-3.9	-3	-4.5 Homo sapiens, Similar to RIKEN cDNA 2810049G06 gene, clone MGC:27268 IMAGE:4818778, mRNA, complete cds	Unpublished	468	910
37	17 others	43849_s_at	HG-U95B	AA622510	NM_138805	NP_620160	LOC131177	3p21.1	-5.2		-2.6			-13.3 Homo sapiens, Similar to RIKEN cDNA 1810037C20 gene, clone MGC:21481 IMAGE:3852082, mRNA, complete cds	Unpublished	469	911
37	17 others	45394_s_at	HG-U95B	AA569333	NM_138805	NP_620160	LOC131177	3p21.1	-4.4		-2.3			-7.1 Homo sapiens, Similar to RIKEN cDNA 1810037C20 gene, clone MGC:21481 IMAGE:3852082, mRNA, complete cds	Unpublished	469	911
38	17 others	46030_at	HG-U95B	AA428560	NM_033197	NP_149974	MGC14597	20q11.21		-3.1	-3.7		-8.5	-5.4 von Ebner minor salivary gland protein	Unpublished	470	912
39	17 others	49811_at	HG-U95B	N21741	NM_016583, NM_130852	NP_057807 NP_570913	LOC51297	20q11.2	-6.1	-4		-3.8	-13.4	-24.3 LUNX protein; PLUNC (palate lung and nasal epithelium clone); tracheal epithelium enriched protein	Biochim. Biophys. Acta 1493:383-387 (2000)	471, 472	913, 914
40	17 others	51685_r_at	HG-U95B	AA583578	NM_032289	NP_115488	MGC14128	8q24.13	-2.8	-2.2	-4.4	-2.1	-3	-9 ESTs, Moderately similar to alternatively spliced product using exon 13A [H.sapiens]	Unpublished	473	915
41	20 protein binding protein	48271_at	HG-U95B	AI753747	NM_004117	NP_004108	FKBP5	6p21.3-p21.2			-2.3			-21.2 FK506-binding protein 5	J. Biol. Chem. 268:18385-18371 (1993)	474	916
42	20 protein binding protein	54152_at	HG-U95B	AI026868	NM_004095	NP_004086	EIF4EBP1	8p12	-2.8		-7.3	-2.3	-2.7	eukaryotic translation initiation factor 4E binding protein 1	Nature 371:762-767 (1994)	475	917

Table 32

	Cat_1 category tag	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lgt.1 Day 3 AI	lgt.1 Day 7 IMM	lgt.1 Day 7 AI	lgt.2 Day 3 AI	lgt.2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
43	25	structural protein	44730_at	HG-U95B	AA788946	NM_004370 NM_080845	NP_004381 NP_542376	COL12A1	8q12-q13		-2.9	-3.5		-6.8	collagen, type XII, alpha 1	Proc. Natl. Acad. Sci. U.S.A. 84:5240-5244 (1987)	478, 477	918, 916

	Cat_1 category tag	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lgt.1 Day 3 AI	lgt.1 Day 7 IMM	lgt.1 Day 7 AI	lgt.2 Day 3 AI	lgt.2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
44	26	transcription factor	42769_at	HG-U95B	N45441	NM_003709	NP_003700	KLF7	2q34		-2.2		-2.5	-3.7	-5.7	-4.7	Kruppel-like factor 7 (ubiquitous) / ESTs	J. Biol. Chem. 273:(43), 28229-28237 (1998)	476	916

	Cat_1 category tag	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lgt.1 Day 3 AI	lgt.1 Day 7 IMM	lgt.1 Day 7 AI	lgt.2 Day 3 AI	lgt.2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
45	27	transporter	43826_at	HG-U95B	AA044844	NM_014585	NP_055400	SLC11A3	2q32		-2.3	-3.3		-2.5	-3.8		solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3	-	479	917
46	27	transporter	47575_s_at	HG-U95B	AA044244	NM_002247	NP_002238	KCNMA1	10q22			-5.2		-3.3	-7		potassium large conductance calcium-activated channel, subfamily M, alpha member 1	Science 261:221-224 (1993)	480	922
46	27	transporter	53788_at	HG-U95B	AI819282	NM_002247	NP_002238	KCNMA1	10q22			-2.8	-3	-4.8	-6.1		potassium large conductance calcium-activated channel, subfamily M, alpha member 1	Science 261:221-224 (1993)	480	922
47	27	transporter	48048_at	HG-U95B	AI587292	NM_006424	NP_006415	SLC34A2	4p15.3-p15.1	-2.8		-2		-4.3	-4.3		solute carrier family 34 (sodium phosphate), member 2	Biochem. Biophys. Res. Commun. 258:578-582 (1999)	481	923
48	27	transporter	51261_at	HG-U95B	AI052920	NM_022153 NM_080594	NP_071047 NP_542131	BPGM	7q31-q34	-4		-3.7		-2.5	-2.4		2,3-bisphosphoglycerate mutase	Genomics 58:288-304 (1999)	482, 483	924, 925

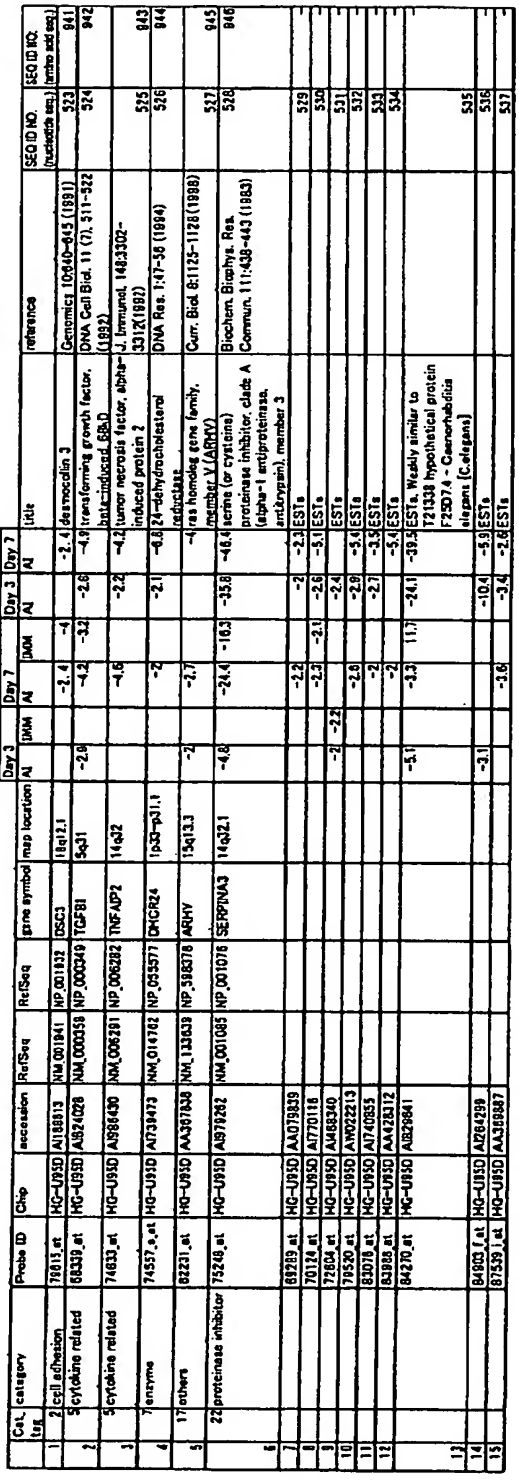
Table 33

	Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	1st 1 Day 3 AI	1st 1 Day 3 IMM	1st 1 Day 7 AI	1st 1 Day 7 IMM	1st 2 Day 3 AI	1st 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
	49		44676_at	HG-U95B	AA434020						-3.4	-1.9		-5.7	-1.1	hypothetical gene supported by AL449243	Genome Res. 8 (9): 897-28 1998	484	-
	50		45694_at	HG-U95B	AL040038					-2.7		-2.3			-4.5	ESTs	Unpublished	485	-
	51		46709_at	HG-U95B	AI807170			SEMA4B	15q23	-2.8		-1.6	-2.2		-2.5	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	Unpublished	486	-
	52		47578_at	HG-U95B	AA190136					-1.4		-4.7		-2.3	-3.1	ESTs	Genome Res. 8 (9): 897-28 1998	487	-
	53		48699_at	HG-U95B	AA398153							-7			-1.8	ESTs	Unpublished	488	-
	54		49819_at	HG-U95B	AI432375					-4.3		-4.5	-6.3	-2.6	-5	ESTs	Unpublished	489	-
	55		49885_at	HG-U95B	AI817802					-1.3				-2.4	-4.1	ESTs	Unpublished	490	-
	56		52394_g_at	HG-U95B	AI924780						-2.8	-2.5		-5.3	-4	EST	Unpublished	491	-
	57		53747_at	HG-U95B	AA422178					-5.3		-2.8			-12.2	Homo sapiens cDNA: FLJ21765 fis, clone COL-F0067	Unpublished	492	-
	58		57282_at	HG-U95B	AA400810							-4.1			-4.1	ESTs	Unpublished	493	-
	59		38328_s_at	HG-U95B	AI760172					-1.3				-2		general transcription factor IIH, polypeptide 3 (34kD subunit)	Unpublished	494	-
	60		59109_at	HG-U95B	AA442232							-2.3			-1.7	ESTs	Unpublished	495	-
	61		59567_at	HG-U95B	AA456093					-2	-2	-2.3	-2.3	-2.1	-3.5	ESTs	Unpublished	496	-

Table 34

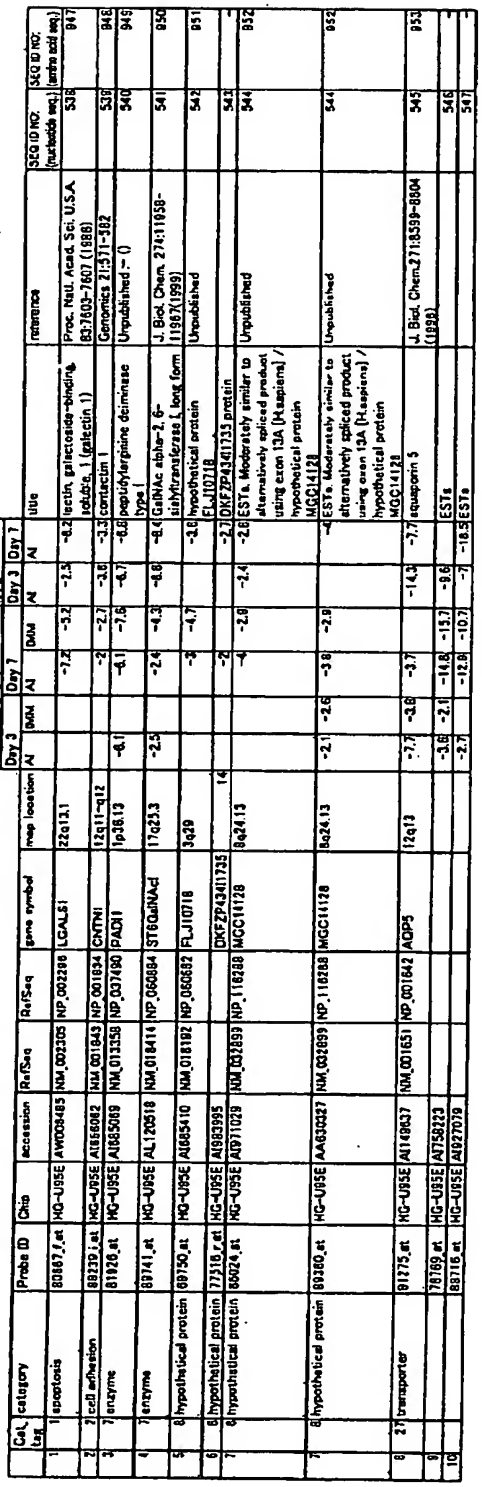
	Cat tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	Int 1 Day 3 AI	Int 1 Day 3 IMM	Int 1 Day 7 AI	Int 2 Day 3 AI	Int 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
1	3	cell cycles	37044_s_at	HG-U95C	AW015590	NM_014059	NP_054778	RGC32	13q13.3	-2.7			-2.7	-2.4	RGC32 protein	Unpublished	497	926
2	4	chemokine	35823_at	HG-U95C	N45415	NM_004887	NP_004878	SCYB14	5q31	-4.1			-2.1	-2.5	small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK)	Biochem. Biophys. Res. Commun. 255:703-706 (1999)	498	927
3	8	hypothetical protein	48793_at	HG-U95C	AA150358	NM_014899	NP_055714	KIAA0878	5q15			-2.8	-2.4	-2.1	KIAA0878 protein	Unpublished	498	928
4	8	hypothetical protein	49188_at	HG-U95C	N62044	NM_017640	NP_060110	FLJ20048	6q22.1	-2.4		-4.3		-2.3	hypothetical protein FLJ20048	Unpublished	500	929
5	8	hypothetical protein	34791_at	HG-U95C	AI820463	NM_032323	NP_115699	MGC13102	1q21.3	-4.6		-3.0	-2.1		hypothetical protein MGC13102	Unpublished	501	930
6	8	hypothetical protein	36214_r_at	HG-U95C	AA053401					-2.5		-3.5	-17	-1.2		Genome Res. 6 (9): 807-28 1996	502	-
7	8	hypothetical protein	40936_at	HG-U95C	AA181265							-2.6		-2.7	ESTs	Genome Res. 6 (9): 807-28 1996	503	-
8	8	hypothetical protein	40940_at	HG-U95C	AA181265							-5.9		-11.6	ESTs	Genome Res. 6 (9): 807-28 1996	503	-
9	8	hypothetical protein	42490_f_at	HG-U95C	AI207832	NM_018050	NP_060520	FLJ10288	12p13.2	-3.7		-4.5	-3.4	-3.4	hypothetical protein FLJ10288	Unpublished	504	931
10	8	hypothetical protein	42972_at	HG-U95C	W56118			KIAA1378	5q14.3		-2.5	-2.2		-3.9	KIAA1378 protein	Unpublished	505	-
11	8	hypothetical protein	44041_at	HG-U95C	AA587248			KIAA1378	5q14.3			-4		-4.1	KIAA1378 protein	Unpublished	506	-
12	8	hypothetical protein	43150_at	HG-U95C	T53027							-2.9	25	-3.5	ESTs, Weakly similar to 138022 hypothetical protein [H.sapiens]	Genome Res. 6 (9): 807-28 1996	507	-
13	8	hypothetical protein	44342_at	HG-U95C	AA150254	NM_016619	NP_057703	LOC51316	4q21.21-q21.23	-2		-2.4		-5	hypothetical protein	Unpublished	508	932
14	8	hypothetical protein	44283_at	HG-U95C	AI030833	-				-3.6	-2.8	-3.6	-1.7	-2.8	ESTs/hypothetical protein FLJ20151	-	509	-
15	8	hypothetical protein	44345_s_at	HG-U95C	AW003533			KIAA1102	4p13	-2.7			-5.6	-1.2	KIAA1102 protein	Unpublished	510	-
16	8	hypothetical protein	45828_at	HG-U95C	AA029458					-2.3	-4.5	-3.4	-3.1	-5.8	Homo sapiens cDNA FLJ11041 fis, clone PLACE1004105	Genome Res. 6 (9): 807-28 1996	511	-
17	8	hypothetical protein	45878_at	HG-U95C	R45447			MGC16207	11q23.3		-4.5	-4	-23	-1.4	hypothetical protein MGC16207	Unpublished	512	-
18	10	kinase	41873_at	HG-U95C	AI741715	NM_000157	NP_000148	GK	Xp21.3			-2.7		-2.1	glycerol kinase	Am. J. Med. Genet. 36:23-28 (1990)	513	933
19	12	membrane protein	43958_at	HG-U95C	AI583077	NM_005672	NP_005663	PSCA	8q24.2	-9.8		-6.5		-9.8	prostate stem cell antigen	Unpublished	514	934
20	17	others	33440_at	HG-U95C	AI828943	NM_016583 NM_130852	NP_057667 NP_570913	LOC51297	20q11.2	-17.3	-10.5	-60.6	-3.7	-10.8	-33.7 LUNX protein; PLUNC (palate lung and nasal epithelium clone); tracheal epithelium enriched protein	Biochem. Biophys. Acta 1493:363-367 (2000)	515, 516	935, 936
21	17	others	33442_g_at	HG-U95C	AI828943	NM_016583 NM_130852	NP_057667 NP_570913	LOC51297	20q11.2	-14	-9.9	-181.3	-126	-14.4	-33.7 LUNX protein; PLUNC (palate lung and nasal epithelium clone); tracheal epithelium enriched protein	Biochem. Biophys. Acta 1493:363-367 (2000)	515, 516	935, 936
22	17	others	63813_at	HG-U95C	AL119458	NM_016023	NP_057109	DREV1	19p13.2-p12	-2			-2.1	-2.1	CGI-81 protein	Unpublished	517	937
23	25	structural protein	62098_at	HG-U95C	AI831452	NM_005555	NP_005546	KRT6B	12q12-q13	-3.4	-3.5	-5.6	-2.5	-5.5	keratin 6B	Proc. Natl. Acad. Sci. U.S.A. 82:4883-4887 (1985)	518	938
24	26	transcription factor	64071_at	HG-U95C	N25612	NM_018660	NP_061130	LOC55893	8q12		-2	-3.5		-2.6	papillomavirus regulatory factor PRF-1	Unpublished	519	939
25	26	transcription factor	64121_at	HG-U95C	Z78373	NM_006530	NP_006521	GAS41	12q13-q15			-2		-2	glioma-amplified sequence-41	Hum. Mol. Genet. 6:1817-1824 (1997)	520	940
26			64143_at	HG-U95C	AI760733							-3.6	-2.3	-3.1	Homo sapiens clone 25104 mRNA sequence	Unpublished	521	-
27			65899_at	HG-U95C	AA203423							-2.6		-4.1	hypothetical protein	Unpublished	522	-

Table 35



	Cat. No.	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	lgt.1 Day 3 AI	lgt.1 Day 3 DMM	lgt.1 Day 7 AI	lgt.1 Day 7 DMM	lgt.2 Day 3 AI	lgt.2 Day 7 AI	title	reference	SEQ ID NO. (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
1	2	cell adhesion	78813_at	HG-U95D	AI188813	NM_001841	NP_001832	DSC3	18q12.1			-2.4	-4		-2.4	desmocolin 3	Genomics 10:940-943 (1991)	523	941
2		Scytokine related	68339_at	HG-U95D	AI924026	NM_000358	NP_000349	TGFBI	5q31	-2.8		-4.2	-3.2	-2.8	-4.9	transforming growth factor, beta-induced, 68kD	DNA Cell Biol. 11 (7), 511-522 (1992)	524	942
3		Scytokine related	74633_at	HG-U95D	AI986430	NM_006288	NP_006282	TNFAIP2	14q32			-4.6		-2.2	-4.2	tumor necrosis factor, alpha-induced protein 2	J. Immunol. 148:3302-3312(1992)	525	943
4		Yenzyme	74557_s_at	HG-U95D	AI738473	NM_014762	NP_055577	DHCR24	1p33-p31.1			-2		-2.1	-6.8	24-dehydrocholesterol reductase	DNA Res. 1:47-56 (1994)	526	944
5	17	others	82231_at	HG-U95D	AA387838	NM_133639	NP_598378	ARHV	15q13.3	-2		-1.7			-4	ras homolog gene family, member V (ARHV)	Curr. Biol. 8:1125-1128(1998)	527	945
6	22	proteinase inhibitor	75248_at	HG-U95D	AI979282	NM_001085	NP_001076	SERPINA3	14q32.1	-4.8		-24.4	-10.3	-35.8	-48.4	serine (or cystatine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	Biochem. Biophys. Res. Commun. 111:438-443 (1983)	528	946
7			88289_at	HG-U95D	AA079839							-2.2		-2	-2.3	ESTs		529	-
8			70124_at	HG-U95D	AI770116							-2.3	-2.1	-2.6	-5.1	ESTs		530	-
9			72604_at	HG-U95D	AI468340					-2	-2.2			-2.4		ESTs		531	-
10			78520_at	HG-U95D	AW022213							-2.6		-2.9	-5.4	ESTs		532	-
11			83078_at	HG-U95D	AI740855							-2		-2.7	-3.5	ESTs		533	-
12			83988_at	HG-U95D	AA428112							-2			-5.1	ESTs		534	-
13			84270_at	HG-U95D	AI829841					-5.1		-3.3	11.7	-24.1	-39.3	ESTs, Weakly similar to T21338 hypothetical protein F23D7.4 - Caenorhabditis elegans [C.elegans]		535	-
14			84803_f_at	HG-U95D	AI264299					-3.1				-10.4	-5.9	ESTs		536	-
15			87539_i_at	HG-U95D	AA369887							-1.6		-3.4	-2.9	ESTs		537	-

Table 36



	Cat. tag	category	Probe ID	Chip	accession	RefSeq	RefSeq	gene symbol	map location	1st 2 Day 3 AI	1st 2 Day 3 DMM	1st 2 Day 7 AI	1st 2 Day 7 DMM	1st 2 Day 7 AI	title	reference	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
1	1	apoptosis	80867_at	HG-U95E	AW008485	NM_002305	NP_002296	LGALS1	22q13.1			-7.2	-3.2	-2.5	-6.2 lectin, galactoside-binding, soluble, 1 (galectin 1)	Proc. Natl. Acad. Sci. U.S.A. 85:7603-7607 (1988)	538	947
2	2	cell adhesion	88239_at	HG-U95E	AI656042	NM_001843	NP_001834	CNTN1	12q11-q12			-2	-2.7	-3.6	-3.3 contactin 1	Genomics 21:371-382	539	948
3	3	enzyme	81928_at	HG-U95E	AI865069	NM_013358	NP_037490	PADI1	1p36.13	-6.1		-6.1	-7.6	-6.7	-6.6 peptidylarginine deiminase type I	Unpublished :- ()	540	949
4	3	enzyme	88741_at	HG-U95E	AL120518	NM_018414	NP_060884	ST6GalNAc1	17q25.3	-2.5		-2.4	-4.3	-4.8	-6.4 GalNAc alpha-2, 6-sialyltransferase I, long form	J. Biol. Chem. 274:11958-11967(1999)	541	950
5	6	hypothetical protein	89750_at	HG-U95E	AI865410	NM_018192	NP_060662	FLJ10718	3q29			-3	-4.7		-3.8 hypothetical protein FLJ10718	Unpublished	542	951
6	6	hypothetical protein	77318_r_at	HG-U95E	AI983995			DKFZP434I1735	14			-2			-2.7 DKFZP434I1735 protein		543	-
7	6	hypothetical protein	86024_at	HG-U95E	AI971029	NM_032899	NP_116288	MGC14128	8q24.13			-4	-2.8	-2.4	-2.8 ESTs, Moderately similar to alternatively spliced product using exon 13A (H.sapiens) / hypothetical protein MGC14128	Unpublished	544	952
8	6	hypothetical protein	89360_at	HG-U95E	AA630327	NM_032899	NP_116288	MGC14128	8q24.13	-2.1	-2.6	-3.8	-2.8		-4 ESTs, Moderately similar to alternatively spliced product using exon 13A (H.sapiens) / hypothetical protein MGC14128	Unpublished	544	952
9	27	transporter	81775_at	HG-U95E	AI140637	NM_001651	NP_001642	AQP5	12q13	-7.7	-3.8	-3.7		-14.3	-7.7 aquaporin 5	J. Biol. Chem.271:8599-8604 (1996)	545	953
10			78769_at	HG-U95E	AI758223					-3.6	-2.1	-14.8	-15.3	-9.6	ESTs		546	-
			88716_at	HG-U95E	AI927079					-2.7		-12.8	-10.7	-7	-18.5 ESTs		547	-

[0191] RefSeq gene sequences on the chips of HG-U95A to HG-U95E and the amino acid sequences thereof, and,

if RefSeq genes are unavailable, EST sequences, are shown in the Sequence Listing.

2. Pendrin gene

[0192] Among the sequences whose expression levels change in response to IL-13 stimulation in both Lots 1 and 2 in the respiratory epithelial cells cultured by the AI method, the pendrin gene (RefSeq: NM_000441 and NM_000432; SEQ ID NOs: 2 and 3) was selected by the analysis described above, as a gene whose expression level was increased on day 3 and day 7 by a factor of ten or more. The Pendrin gene belongs to the category of transporters. In respiratory epithelial cells cultured with the IMM method, the expression level of the pendrin gene was also found to be increased by a factor of 20 or more in response to IL-13 stimulation on day 3 and day 7 in both Lots 1 and 2.

[0193] This gene is closely associated with allergies induced by IL-13 stimulation. The analysis result for the pendrin gene obtained using HG-U95A chip is shown in Table 37.

Table 37

		Lot 1				Lot 2	
		Day 3	Day 7	Day 3	Day 7	Day 3	Day 7
Probe set ID	Accession	AI	IMM	AI	IMM	AI	AI
36376_at	AF030880	18.8	25.6	20.1	28.5	118.3	58.2

[0194] The PDS gene is a causative gene of the hereditary disease Pendred's syndrome, which is characterized by congenital deafness and goiters (Everett L. A. et al., Nat. Genet. 17: 411-22 (1997)). The gene was reported as a sulfuric acid transporter, because of the presence of a sulfuric acid transporter domain. However, after the report, the protein has been studied as a protein that transports other anions such as Cl^- and I^- (Scott D. A. et al . , Nat. Genet. 21(4): 440-3 (1999); Scott D.A. and Karniski L. P., Am. J. Physiol. 278: C207-11 (2000)). Pendrin is an 86-kDa transmembrane protein that consists of 780 amino acid residues and has a 12 transmembrane domain. In humans, the gene has been found to be expressed in the inner ear and thyroid gland at high levels, and in the kidney, endometrium, and placenta at lower levels (Rayaux I.E. et al., Endocrinology 141: 839-45 (2000) ; Bidart J. M. et al. , J. Clin. Endocrinol. Metab. 85: 2028-33 (2000)). On the other hand, in mice and rats, the gene is expressed in the kidney at a high level, and the expression is also detectable in the endometrium and placenta. The PDS gene encoding pendrin has been mapped on chromosome 7q31 , the location of the DFNB4 locus. The causative gene of congenital colon disorder, DRA (SLC26A3; down-regulated in colonic adenoma), has been mapped immediately downstream of the PDS gene in an inverse configuration.

[0195] The DRA gene encodes a sulfur transporter that is expressed at high levels in the colon and mucous membranes, and the transporter is structurally very similar to pendrin. Another gene exhibiting a high similarity to the PDS gene is DTDST (SLC26A2; diastrophic dysplasia) that is a causative gene of diastrophic dysplasia, which has been mapped on chromosome 5q32-q33.1. DTDST is also known to encode a protein functioning as a sulfur transporter. PDS gene knockout mice are deaf and are affected with vestibular function disorders. The inner ears are normal in 15-day olds or younger fetuses, but enlargement, sensory cell deformities , and otocranial deformities are developed after that (Everett L. A. et al., Hum. Mol. Genet. 10(2): 153-61 (2001)) .

EXAMPLE 6

Determination of the expression levels of candidate genes in bronchial epithelial cells cultured by the AI method or the IMM method

[0196] Quantitative PCR assays were further performed with ABI 7700 using two batches of epithelial cells cultured respectively by the AI method and the IMM method described in Example 1 to quantitatively determine the expression level of the pendrin gene selected in Example 5. The primers and TaqMan probe used in the assays with ABI 7700 were designed based on the information on the sequence of the pendrin gene utilizing Primer Express (PE Biosystems). The 5' and 3' ends of the TaqMan probe were labeled with FAM (6-carboxy-fluorescein) and TAMRA (6-carboxy-N,N,N',N'-tetramethylrhodamine), respectively. The sequences of oligonucleotides of the forward primer (F), reverse primer (R) , and TaqMan probe (TP) for the pendrin gene are shown below. The GenBank accession number corresponding to the nucleotide sequence of each marker gene is shown in parenthesis after the name. Pendrin (AF030880)

DOCID: <EP_____1394274A2_I_>

F: TTTGCCTCCTGAACTTCCACC (SEQ ID NO: 4)

R: CCTACTGACACTGCAATAGCATAAGC (SEQ ID NO: 5)

TP: cttgttctcggagatgctggctgcat (SEQ ID NO: 6)

[0197] Total RNA extracted by the aforementioned method was treated with DNase (Nippon Gene). Then, cDNA, which was reverse transcribed using random hexamer (GIBCO BRL) as primer, was used as a template. For a standard curve to calculate the number of copies, a plasmid clone containing a nucleotide sequence region that is amplified by both primers was prepared for each of the genes, and this was diluted stepwise to be used as template for carrying out the reaction. The composition of reaction solution for monitoring PCR amplification is shown in Table 38.

Table 38

Composition of reaction in ABI-PRISM 7700 (Amount per well)	
Sterilized distilled water	23.75 (μL)
10x TaqMan buffer A	5
25mM $MgCl_2$	7
dATP(10 mM)	1.0
dCTP(10 mM)	1.0
dGTP(10 mM)	1.0
dUTP (20 mM)	1.0
Forward Primer (10 μM)	1.0
Reverse Primer (10 μM)	1.0
TaqMan probe (2.0 μM)	2.5
AmpliTaq Gold (5 U/μL)	0.25
AmpErase UNG (1 U/μL)	0.5
Template solution	5
Total	50

[0198] Additionally, to correct the differences of cDNA concentration in the sample, a similar quantitative analysis was performed for β-actin gene and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene as internal standards for correction. By correcting based on the number of copies of these genes, the number of copies of the genes of interest was calculated.

[0199] Primers and probes for measuring β-actin or GAPDH were designed from Primer Express (Applied Biosystems) based on the genetic information of each gene. The nucleotide sequences are as shown below. The β-actin-corrected expression levels (copy/5 ng RNA) for marker genes are shown in Figs. 3.

β-actin forward primer (SEQ ID NO: 7)
TCA CCC ACA CTG TGC CCA TCT ACG A

β-actin reverse primer (SEQ ID NO: 8)
CAG CGG AAC CGC TCA TTG CCA ATG G

β-actin TaqMan probe (SEQ ID NO: 9)
(FAM) ATGCCCTCCCCCATGCCATCCTGCGT (TAMRA)-3'

GAPDH forward primer (SEQ ID NO: 10)
GAAGGTGAAGGTCGGAGT

GAPDH reverse primer (SEQ ID NO: 11)
GAAGATGGTGATGGGATTTC

GAPDH TaqMan probe (SEQ ID NO: 12)
(FAM) CAAGCTTCCCGTTCTCAGCC (TAMRA) -3'

FAM: 6-carboxy-fluorescein
TAMRA: 6-carboxy-N,N,N',N'-tetramethylrhodamine

[0200] As a result of quantitative PCR, the expression level of the pendrin gene (selected in Example 5) in the respiratory tract epithelial cells was elevated by hundred folds or more as a result of IL-13 stimulation in respiratory tract epithelial cells when cultured according to the AI method or IMM method. Based on these results, it was presumed that the expression level of the marker gene was elevated in respiratory tract epithelial cells in response to IL-13.

[0201] The marker genes of this invention show common behavior among different lots of bronchial epithelial cells by IL-13 stimulation known to have a close relationship to allergic reactions. Therefore, the marker genes of this invention are thought to be important genes that regulate the progression of allergic reactions.

EXAMPLE 7

RNA recovery from the lung of OVA antigen-exposed bronchial hypersensitivity mouse model

[0202] The OVA antigen-exposed bronchial hypersensitivity model has been reported as a bronchial asthma model. 50 μg OVA and 1 mg aluminum hydroxide (an adjuvant) were injected into the peritoneal cavity of Balb/c mice (male, seven-week old), and after 10 days the mice was sensitized with OVA under the same conditions. Then, after 10 days, 1% OVA was given by inhalation using the Ultra-nebulizer model UN701 (Azwell(Co., Ltd.)) for 30 minutes every four days three times in total. Enhanced bronchial hypersensitivity was monitored by detecting the respiratory constriction caused by acetylcholine (6.25-2000 μg/kg) using an artificial respirator (model 131, New England Medical Instruments Inc.) 24 hours after the final antigen inhalation (Nagai H. et al, Int Arch Allergy Immunol; 108: 189-195, 1995) . Bronchial hypersensitivity can be induced by this treatment.

[0203] Variations in the expression level of the mouse pendrin gene were studied using RNA from the lungs of this model.

[0204] The test was conducted using the following four groups: OVA antigen-exposed bronchial hypersensitivity group (called the "S-OVA group"; N=7)); and three control groups: untreated group (called the "naive group";(N=6)); physiological saline-inhaled group to which the OVA antigen was given twice for immunization and physiological saline was given by inhalation (called the "S-Sal group"; (N=6)); and the Prednisolone-administered group, to which Prednisolone was given by inhalation 10 times in total from the day before antigen inhalation until the final antigen inhalation, and the development of bronchial hypersensitivity was suppressed by giving 5 mg/kg Prednisolone orally (called the "Pred-group"; (N=7)).

[0205] The left lungs were removed 24 hours after the antigen was inhaled three times, by which time, the symptoms of bronchial hypersensitivity can be seen. The lung tissues were dissolved in 2 ml of Isogen (Nippon Gene; Wako Pure Chemical Industries) and immediately crushed with the homogenizer DIAX100 (Heidolph). RNA was isolated from 1 ml of this solution according to the protocol attached to Isogen. Chloroform was added to the solution. After the mixture was stirred and centrifuged, the aqueous layer was recovered. Then, isopropanol was added. After the mixture was stirred and centrifuged, the precipitated total RNA was collected. Total RNAs (approximately 20-60 μg) were extracted from the samples of the four groups (N=26) described above.

EXAMPLE 8

Determination of the expression level of pendrin gene in the lung of OVA antigen-exposed bronchial hypersensitivity model

[0206] Quantitative PCR assay was performed with ABI 7700 using the lung RNAs described in Example 8 to quantitatively determine the expression level of the mouse pendrin gene (RefSeq: NM_011867, NM_035997, SEQ ID NO: 13/DNA, and SEQ ID NO: 14/amino acid sequence). The primers and TaqMan probe used in the assay with ABI 7700 were designed based on the information on the sequence of the pendrin gene utilizing Primer Express (Applied Bio Systems). The 5' and 3' ends of the TaqMan probe were labeled with FAM (6-carboxy-fluorescein) and TAMRA (6-carboxy-N,N,N',N'-tetramethylrhodamine), respectively. The sequences of oligonucleotides of the forward primer (F) , reverse primer (R) and TaqMan probe (TP) for the pendrin gene are shown below. The GenBank accession number corresponding to the nucleotide sequence of the mouse pendrin gene is shown in parenthesis after the name.

mouse pendrin (AF167411)

F: GGTTCTTGCCTCCTGTCCTG (SEQ ID NO: 15)

R: AATGGAAAAGGATGCAGCCA (SEQ ID NO: 16)

TP: catctgtgggcctgttttcggacatg (SEQ ID NO: 17)

[0207] Total RNA extracted by the aforementioned method was treated with DNase (Nippon Gene). Then, cDNA, which was reverse transcribed using random hexamer (GIBCO BRL) as primer, was used as a template. For a standard curve to calculate the number of copies, a plasmid clone comprising a nucleotide sequence region that is amplified by both primers was prepared for each of the genes, and this was diluted stepwise to be used as a template for carrying out the reaction. The composition of the reaction solution for monitoring PCR amplification is shown in Table 39.

Table 39

Composition of the reaction solution in ABI-PRISM 7700 (Amount per well)	
Sterilized distilled water	23.75 (μL)
10x TaqMan buffer A	5
25mM $MgCl_2$	7
dATP(10 mM)	1.0
dCTP(10 mM)	1.0
dGTP(10 mM)	1.0
dUTP (20 mM)	1.0
Forward Primer (10 μM)	1.0
Reverse Primer (10 μM)	1.0
TaqMan probe (2.0 μM)	2.5
AmpliTaq Gold (5 U/μL)	0.25
AmpErase UNG (1 U/μL)	0.5
Template solution	5
Total	50

[0208] Additionally, to correct the differences of cDNA concentration in the sample, a similar quantitative analysis was performed for mouse β-actin gene and mouse glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene as internal standards for correction. By correcting based on the number of copies of these genes, the number of copies of the genes of interest was calculated.

[0209] Primers and probes for measuring mouse β-actin or mouse GAPDH were designed from Primer Express (Applied Biosystems) based on the genetic information of each gene. The nucleotide sequences are as shown below. The mouse β-actin-corrected expression levels (copy/5 ng RNA) for each of the genes are shown in Fig. 4.

mouse β-actin forward primer (SEQ ID NO: 18)
ACTATTGGCAACGAGCGGTTC

mouse β-actin reverse primer (SEQ ID NO: 19)

GGATGCCACAGGATTCCATACC

mouse β-actin TaqMan probe (SEQ ID NO: 20)
(FAM) CCTGAGGCTCTTTTCCAGCCTTCCTTCT (TAMRA) -3'

mouse GAPDH forward primer (SEQ ID NO: 21)
GCACCACCAACTGCTTAGCC

mouse GAPDH reverse primer (SEQ ID NO: 22)
CTTTGGCATTGTGGAAGGGCTCATG

mouse GAPDH TaqMan probe (SEQ ID NO: 23)
(FAM) GATGCAGGGATGATGTTCTGG (TAMRA)-3'

FAM: 6-carboxy-fluorescein
TAMRA: 6-carboxy-N,N,N',N'-tetramethylrhodamine

[0210] According to the result of quantitative PCR, the expression level in the lung of OVA antigen-exposed bronchial hypersensitivity mice was about 50 times higher than that in the lung of physiological saline-inhaled mice. This finding suggests that the pendrin gene may be an important gene that controls the progression of allergic reactions, particularly asthma because the gene is expressed at a higher level in the lung of OVA antigen-exposed bronchial hypersensitivity model mouse that mimics human asthma.

EXAMPLE 9

Determination of the localization of pendrin mRNA in the lung of OVA antigen-exposed bronchial hypersensitivity model by *in situ* hybridization (hereinafter referred to as "ISH")

[0211] After perfusion fixation with 10% buffered neutral formalin, the pulmonary tissues were collected from three mice each of the four groups (the untreated group; the physiological saline-inhaled group; the Prednisolone-administered group; and the OVA antigen-inhaled group) used in Example 9. The tissues were fixed with 10% buffered neutral formalin, and then embedded in paraffin to prepare tissue blocks.

[0212] All paraffin blocks from the mouse lung samples were sliced into 7 μm sections. Then, the sections were treated with hematoxylin for nuclear staining. Among the sections, sections exhibiting good tissue morphology were selected from a single individual each of the physiological saline-inhaled group and OVA antigen-inhaled group. The sections were tested by ISH. The nucleotide sequence of the ISH probe is shown in SEQ ID NO: 24.

[0213] The paraffin sections of mouse lung tissues from the physiological-saline-inhalation group and the OVA-antigen-inhalation group were rehydrated by deparaffinization (washed with water after treatment with xylene, 100%, 90%, 80%, and 70% alcohol). Then, the sections were treated with the above probe. After the staining, the sections were treated for nuclear staining. The condition used for the ISH experiments is described below. The result of ISH is

shown in Fig. 5.

Probe concentration: 250 ng/ml
hybridization temperature: 60°C
Duration of hybridization: 6 hours
Post-hybridization wash: 0.1x SSC/70°C /6 minutes/3 times
Coloring reagents: NBT/BCIP
Duration of color development: 7 hours

[0214] The ISH result showed that the mouse lung sections from the OVA antigen inhalation group gave a specific staining pattern with the antisense probe. Blue deposits were detectable in the bronchia, bronchiole and macrophages in the pulmonary alveoli. Blue deposits with similar intensity were also found on the epithelial cells of bronchial mucosa. The sense probe resulted in no deposits.

EXAMPLE 10

PAS staining and Alcian Blue staining of lung tissues of OVA antigen-exposed bronchial hypersensitivity model

[0215] The localization of the huge glycoprotein mucin in the lung tissue of OVA antigen-exposed bronchial hypersensitivity model was confirmed by PAS staining for acidic sugar chains and Alcian Blue staining for basic sugar chains. The paraffin blocks of mouse lung tissues from the physiological-saline-inhalation group and the OVA-antigen-inhalation group used in Example 10 were sliced into 3-μm sections. After being rehydrated by deparaffinization (washed with water after treatment with xylene, 100%, 90%, 80% and 70% alcohol) , the sections were treated by PAS staining and Alcian Blue staining. The result obtained by the staining is shown in Fig. 6. The reaction conditions used are as follows:

PAS staining:

1% periodate solution for 10 minutes
washing with water for 5 minutes
cold Schiff's reagent for 15 minutes
sulfuric water for 2 minutes 3 times
washing with water

Alcian Blue staining:

3% acetic acid for 1 minute
Alcian Blue staining solution (pH 2.5) for 30 minutes
3% acetic acid; washing five times
washing with water
dehydration, clearing and mounting
70% alcohol for 5 minutes
80% alcohol for 5 minutes
90% alcohol for 5 minutes
100% alcohol for 5 minutes twice
xylene for 5 minutes twice
xylene type mounting agent; mounting with cover glasses

[0216] Both PAS staining and Alcian Blue staining resulted in positive reactions in the cytoplasmic granules in epithelial cells and goblet cells of bronchial mucosal membrane. This indicates that the epithelial cells and goblet cells of bronchial mucosal membrane contain mucin. According to the results obtained in Examples 12 and 13, the pendrin mRNA are localized in the epithelial cells and goblet cells of bronchial mucosal membrane.

EXAMPLE 11

Variations in the expression levels of marker genes in bronchial hypersensitivity model mouse

1. RNA recovery from the lung of OVA antigen-exposed bronchial hypersensitivity model mouse

[0217] As mentioned above, the OVA antigen-exposed bronchial hypersensitivity model using 7-week old male Balb/

c mice has been reported to mimic human asthma. This mouse model is prepared as described in Example 7. In such mice, bronchial hypersensitivity is enhanced after the final antigen inhalation. Thus, symptoms quite similar to those of asthma can be induced in this model.

[0218] In this Example, RNAs were isolated from the lung and trachea 24 hours after the first, second or third exposure to OVA antigen, and cDNA and cRNA were synthesized from the RNAs. The respective samples were analyzed using a mouse GeneChip (MG-U74A-C), and the result obtained was compared to that from the human goblet cell differentiation model.

[0219] RNAs were isolated from the lung and trachea 24 hours after the first, second and third exposure to OVA antigen. The test was conducted using the following four groups: OVA antigen-inhaled bronchial hypersensitivity group (S-OVA); the three control groups: untreated group (naive) ; physiological saline-inhaled group in which OVA antigen was given twice for immunization and physiological saline was given by inhalation (S-Sal); and Prednisolone-treated group, in which Prednisolone was given by inhalation 10 times in total from the day before antigen inhalation until the final antigen inhalation, and the development of bronchial hypersensitivity was suppressed by giving 5 mg/kg Prednisolone orally (Pred).

[0220] The lung and trachea were resected 24 hours after the first, second and third exposure to OVA antigen. Each tissue was crushed with a homogenizer called Polytrone immediately after dissolving in Isogen (Nippon Gene; Wako Pure Chemical Industries). RNA was isolated from 1 ml of this solution according to the protocol attached to Isogen. Chloroform was added to the solution. After the mixture was stirred and centrifuged, the aqueous layer was recovered. Then, isopropanol was added to the aqueous solution obtained. After the mixture was stirred and centrifuged, the precipitated total RNA was collected. Total RNAs (approximately 20-60 μg) were extracted from the samples of the twelve groups described above.

2. Synthesis of cRNA for GeneChip

[0221] Biotinylated cRNA was synthesized by the same method as described in Example 4. About 20-50 μg biotinylated cRNAs were synthesized from the cDNAs obtained from the twelve groups described above. The cRNAs were purified using RNeasy Spin column (QIAGEN) , and then converted into fragments by heat treatment. A 15-μg aliquot of each cRNA was added to a Hybridization Cocktail according to the Expression Analysis Technical Manual. The cocktail is added to an array chip, followed by incubation for hybridization at 45°C for 16 hours. After hybridization, the chip was stained and analyzed by the same procedure as described in Example 4.

3. GeneChip analysis

[0222] Data analysis was performed using Suite 4.0, which is a GeneChip analysis software. Average Intensity (1) and Background Average (2) were determined by Absolute Analysis, and four average values obtained (naive group, S-Sal group, S-OVA group, and Pred group) by subtracting (2) from (1). These four values were used as scale factors for comparison analysis.

[0223] First, absolute analysis was performed to analyze one chip data. Positives and negatives were determined by comparing the fluorescence intensity of perfect match and mismatch of a probe set. Determination of the three categories of Absolute Calls, i.e., P (present) , A (absent) , and M (marginal) , were made by values of Pos Fraction, Log Avg, and Pos/Neg:

Pos Fraction; ratio of positive pairs.
Log Avg; average of the log of fluorescence intensity ratio between probe cells of perfect match and mismatch.
Pos/Neg; ratio of the number of positive pairs and negative pairs.

[0224] Additionally, Average Difference (Avg Diff), which is the average value of the difference in fluorescence intensities between perfect matching and mismatching probe cells, was calculated for each gene.

[0225] Next, Comparison Analysis was performed on two sets of data. For example, comparison was made between S-Sal group and S-OVA group, and the difference in expression levels was ranked as follows.

[0226] Determination of the 5 categories of difference calls, which are I, D, MI, MD, and NC, were made from values of Inc/Dec, Inc Ratio, Dpos-Dneg Ratio, and Log Avg Ratio Change.

Inc: Number of probe pairs that corresponded to S-Sal group and S-OVA group and that were judged to have increased expression levels in S-OVA group.
Dec: Number of pairs judged to have decreased expression levels in S-OVA group.
Inc/Dec: Ratio of the number of pairs judged to be Inc and number of pairs judged to be Dec.
Inc Ratio: Number of pairs judged to be Inc/number of pairs actually used.
Dpos/Dneg Ratio: Ratio between the number of Neg Change subtracted from that of Pos Change, and the number of

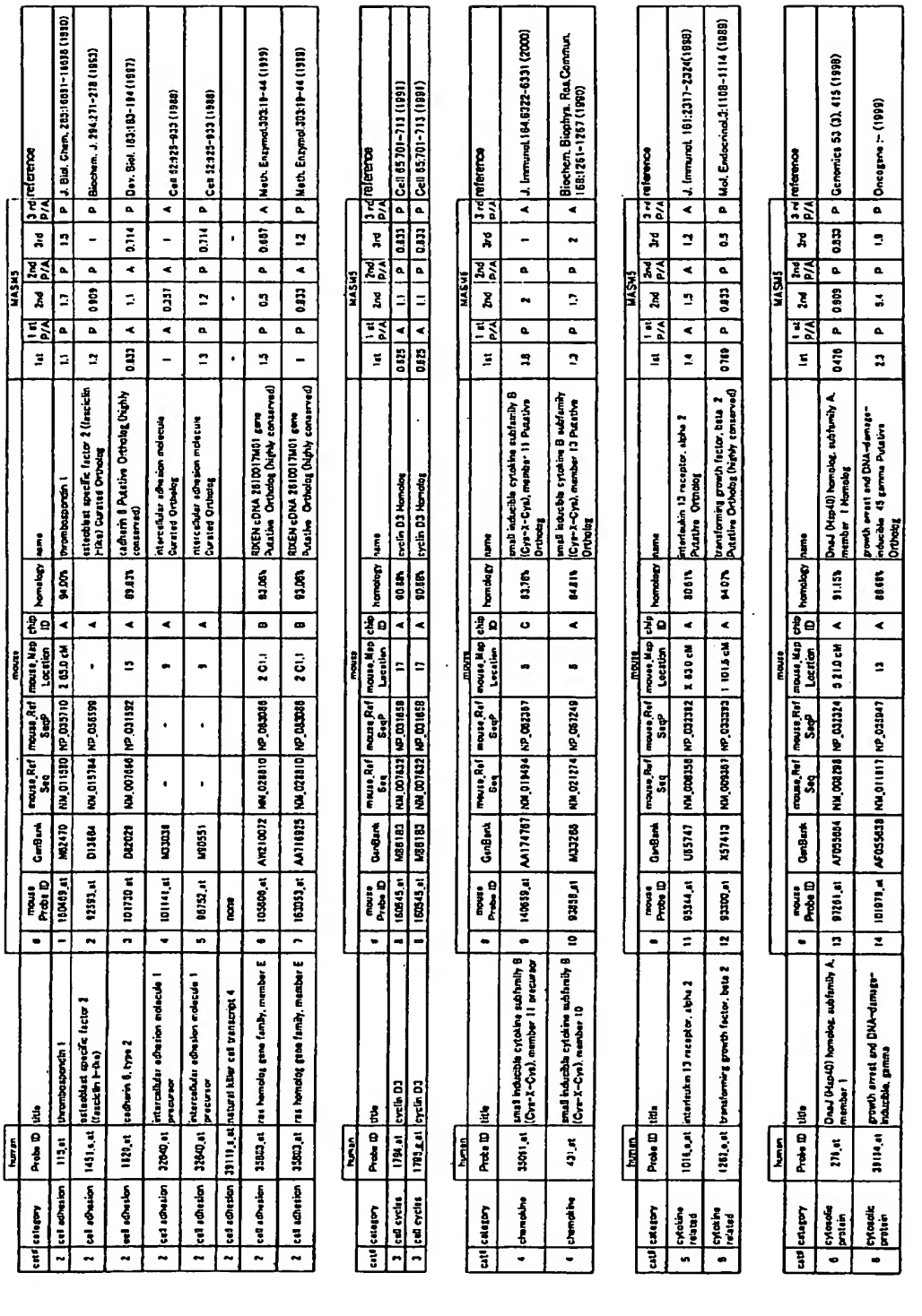
pairs actually used.
Pos Change: Difference between the number of positive pairs in Absolute Analysis of S-Sal group, and the number of positive pairs in Absolute Analysis of S-OVA group.
Neg Change: Difference between the number of negative pairs in Absolute Analysis of S-Sal group, and the number of negative pairs in Absolute Analysis of S-OVA group.
Log Avg Ratio Change: Difference between Log Avg in Absolute Analysis of S-Sal group and S-OVA group.
Increased: I,
Decreased: D,
Marginally Increased: MI,
Marginally Decreased: MD, and
No Change: NC

4. Comparison of a group of genes associated with goblet cell differentiation, which was narrowed down using the chips of HG-U95A to HG-U95E, with a group of genes derived from the OVA antigen-exposed bronchial hypersensitivity model, which was narrowed down using the chips of MG-U74A, MG-U74B, and MG-U74C

[0227] NetAffx database (Affymetrix) was searched for the mouse counterparts of the genes narrowed down using HG-U95A to HG-U95E chips as described above. The Fold Change values are shown in Tables 40 to 83, which were obtained by further analyzing the counterpart genes contained in mouse GeneChip MG-U74A to MG-U74C comparatively between S-Sal group and S-OVA group using Suite4.0 (Affymetrix).

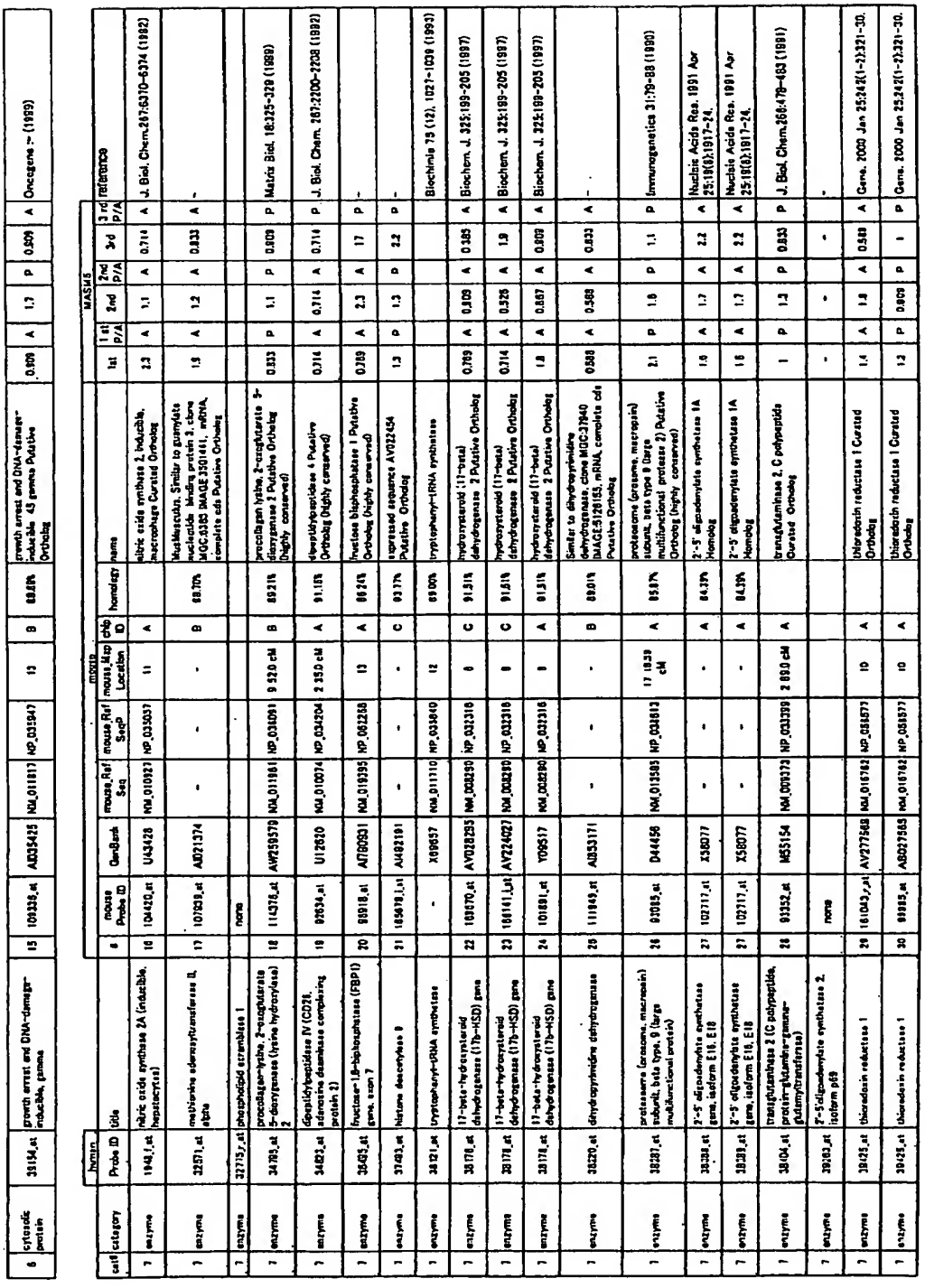
[0228] Based on the expression levels in the mouse asthma model, the genes categorized are shown in Tables 40 to 62 (mouse counterpart genes of the human genes whose expression levels were found to increase by IL-13 under the culture conditions according to the AI method) and Tables 63 to 83 (mouse counterpart genes of the human genes whose expression levels were found to be decreased by IL-13 under the culture condition according to the AI method).

Table 40



cat#	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASS 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
2	cell adhesion	115_at	thrombospondin 1	1	160469_at	M62470	NM_011580	NP_035710	2 65.0 cM	A	94.50%	thrombospondin 1	1.1	P	1.7	P	1.3	P	J. Biol. Chem. 265:16681-16686 (1990)
2	cell adhesion	1451_s_at	osteoblast specific factor 2 (fasciclin I-like)	2	92393_at	D13694	NM_015784	NP_056598	-	A		osteoblast specific factor 2 (fasciclin I-like) Curated Ortholog	1.2	P	0.909	P	1	P	Biochem. J. 294:271-278 (1993)
2	cell adhesion	1822_at	cadherin 6, type 2	3	101720_at	D82029	NM_007666	NP_031392	13	A	89.83%	cadherin 6 Putative Ortholog (highly conserved)	0.833	A	1.1	A	0.714	P	Dev. Biol. 183:183-194 (1997)
2	cell adhesion	32040_at	intercellular adhesion molecule 1 precursor	4	101141_at	M33038	-	-	9	A		intercellular adhesion molecule Curated Ortholog	1	A	0.357	A	1	A	Cell 52:925-933 (1988)
2	cell adhesion	32040_at	intercellular adhesion molecule 1 precursor	5	96152_at	M80551	-	-	9	A		intercellular adhesion molecule Curated Ortholog	1.3	P	1.2	P	0.714	P	Cell 52:925-933 (1988)
2	cell adhesion	39119_s_at	natural killer cell transcript 4		none								-		-		-		
2	cell adhesion	35843_at	ras homolog gene family, member E	6	103609_at	AK210072	NM_028810	NP_083086	2 C1.1	B	93.06%	RIKEN cDNA 2810017M01 gene Putative Ortholog (highly conserved)	1.5	P	0.5	P	0.667	A	Meth. Enzymol.303:19-44 (1999)
2	cell adhesion	35843_at	ras homolog gene family, member E	7	163053_at	AA116825	NM_028810	NP_083086	2 C1.1	B	93.06%	RIKEN cDNA 2810017M01 gene Putative Ortholog (highly conserved)	1	P	0.833	A	1.2	P	Meth. Enzymol.303:19-44 (1999)
3	cell cycles	1794_at	cyclin D3	8	160545_at	M88183	NM_007632	NP_031658	17	A	90.68%	cyclin D3 Homolog	0.625	A	1.1	P	0.833	P	Cell 65:701-713 (1991)
3	cell cycles	1783_s_at	cyclin D3	8	160545_at	M88183	NM_007632	NP_031658	17	A	90.68%	cyclin D3 Homolog	0.625	A	1.1	P	0.833	P	Cell 65:701-713 (1991)
4	chemokine	2501_at	small inducible cytokine subfamily B (Cys-X-Cys), member 11 precursor	9	140619_at	AA174787	NM_019494	NP_062367	8	C	83.76%	small inducible cytokine subfamily B (Cys-X-Cys), member 11 Putative Ortholog	3.8	P	2	P	1	A	J. Immunol.164:6222-6231 (2000)
4	chemokine	431_at	small inducible cytokine subfamily B (Cys-X-Cys), member 10	10	92518_at	M33266	NM_021274	NP_067249	8	A	84.41%	small inducible cytokine B subfamily (Cys-X-Cys), member 10 Putative Ortholog	1.2	P	1.7	P	2	A	Biochem. Biophys. Res. Commun. 168:1261-1267 (1990)
5	cytokine related	1018_s_at	interleukin 13 receptor, alpha 2	11	93344_at	U65747	NM_008358	NP_032382	X 63.0 cM	A	80.61%	interleukin 13 receptor, alpha 2 Putative Ortholog	1.4	A	1.5	A	1.2	A	J. Immunol. 161:2317-2324(1998)
5	cytokine related	1282_s_at	transforming growth factor, beta 2	12	93202_at	X57413	NM_009367	NP_033393	1 101.6 cM	A	94.07%	transforming growth factor, beta 2 Putative Ortholog (highly conserved)	0.769	P	0.833	P	0.5	P	Mol. Endocrinol.3:1108-1114 (1989)
6	cytosolic protein	271_at	DnaJ (Hsp40) homolog, subfamily A, member 1	13	97261_at	AF035694	NM_008298	NP_032324	9 21.0 cM	A	91.15%	DnaJ (Hsp40) homolog, subfamily A, member 1 Homolog	0.476	P	0.909	P	0.833	P	Genomics 53 (3): 415 (1998)
8	Cytosolic protein	39124_at	growth arrest and DNA-damage-inducible, gamma	14	101978_at	AF035638	NM_011817	NP_035947	13	A	88.66%	growth arrest and DNA-damage-inducible 45 gamma Putative Ortholog	2.3	P	5.4	P	1.8	P	Oncogene :- (1999)

Table 41



6	cytosolic protein	35154_at	growth arrest and DNA-damage-inducible, gamma	15	109338_at	AB035425	NM_011817	NP_035947	12	B	88.88%	growth arrest and DNA-damage-inducible 45 gamma Putative Ortholog	0.806	A	1.7	P	0.809	A	Oncogene ~ (1999)

human					mouse								MAS45							
cell	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse Ref Seq	mouse Ref Seq	mouse Map Location	chb ID	homolgy	name	hit	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
?	enzyme	1948_f_at	fabric acids synthase 2A (inducible, hepatocytes)	16	109410_at	U43428	NM_010037	NP_035037	11	A		fabric acids synthase 2, inducible, macrophage Curated Ortholog	2.3	A	1.1	A	0.714	A	J. Biol. Chem.267:6370-6374 (1992)
?	enzyme	33571_at	methionine adenosyltransferase II, alpha	17	107239_at	AB021374	-	-	-	B	88.70%	MusMasculin. Similar to guanylate nucleotide binding protein 3, clone MGC:5180 IMAGE:3501141, mRNA, complete cds Putative Ortholog	1.8	A	1.2	A	0.833	A	-
?	enzyme	32715_at	phosphatidyl scramblase 1		none														
?	enzyme	34783_at	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	18	111378_at	AW259370	NM_011881	NP_036091	9 32.0 cM	B	89.21%	procollagen lysine, 2-oxoglutarate 5-dioxygenase 1 Putative Ortholog Highly conserved	0.833	P	1.1	P	0.809	P	Matrix Biol. 18:325-329 (1999)
?	enzyme	34823_at	dipeptidyl peptidase IV (CD26, adenosine deaminase complexing protein 2)	19	97634_at	U12820	NM_010074	NP_034204	2 35.0 cM	A	91.18%	dipeptidyl peptidase 4 Putative Ortholog Highly conserved	0.714	A	0.714	A	0.714	P	J. Biol. Chem. 267:2200-2208 (1992)
?	enzyme	35403_at	fructose-1,6-biphosphatase (FBP1) gene, exon 7	20	99818_at	AF000331	NM_019395	NP_062258	13	A	88.24%	fructose biphosphatase 1 Putative Ortholog Highly conserved	0.789	A	2.3	A	1.7	P	-
?	enzyme	31403_at	histone deacetylase 9	21	105478_i_at	AA021191	-	-	-	C	93.17%	repressed sequence AV012454 Putative Ortholog	1.3	P	1.3	P	2.2	P	-
?	enzyme	36121_at	tryptophanyl-tRNA synthetase		-	X06657	NM_011110	NP_035240	12		69.00%	tryptophanyl-tRNA synthetase							Biochimie 75 (12), 1027-1029 (1993)
?	enzyme	35178_at	17-beta-hydroxysteroid dehydrogenase (17b-HSD) gene	22	109370_at	AV028295	NM_008290	NP_032316	9	C	91.31%	hydroxysteroid (17-beta) dehydrogenase 2 Putative Ortholog	0.789	A	0.805	A	0.585	A	Biochem. J. 325:199-205 (1997)
?	enzyme	35178_f_at	17-beta-hydroxysteroid dehydrogenase (17b-HSD) gene	23	109141_f_at	AY224027	NM_008290	NP_032316	9	C	91.31%	hydroxysteroid (17-beta) dehydrogenase 2 Putative Ortholog	0.714	A	0.526	A	1.9	A	Biochem. J. 325:199-205 (1997)
?	enzyme	35178_r_at	17-beta-hydroxysteroid dehydrogenase (17b-HSD) gene	24	101691_at	Y09617	NM_008290	NP_032316	9	A	91.31%	hydroxysteroid (17-beta) dehydrogenase 2 Putative Ortholog	1.8	A	0.667	A	0.809	A	Biochem. J. 325:199-205 (1997)
?	enzyme	35220_at	dihydropyrimidine dehydrogenase	25	111849_at	AB033171	-	-	-	B	89.01%	Similar to dihydropyrimidine dehydrogenase, clone MGC:27940 IMAGE:5126153, mRNA, complete cds Putative Ortholog	0.588	A	0.588	A	0.833	A	-
?	enzyme	35237_at	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protein)	26	91035_at	D44456	NM_013585	NP_038613	17 19.0 cM	A	95.87%	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional protease 2) Putative Ortholog (highly conserved)	2.1	P	1.6	P	1.1	P	Immunogenetics 31:79-88 (1990)
?	enzyme	35238_at	2'-5' oligoadenylate synthetase gene, isoform E18, E18	27	102717_at	X58077	-	-	-	A	84.37%	2'-5' oligoadenylate synthetase 1A Homolog	1.8	A	1.7	A	2.2	A	Nucleic Acids Res. 1991 Apr 25:1963:1917-24.
?	enzyme	35238_i_at	2'-5' oligoadenylate synthetase gene, isoform E18, E18	27	102717_at	X58077	-	-	-	A	84.37%	2'-5' oligoadenylate synthetase 1A Homolog	1.8	A	1.7	A	2.2	A	Nucleic Acids Res. 1991 Apr 25:1963:1917-24.
?	enzyme	35104_at	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	28	91352_at	M55154	NM_009373	NP_033399	2 89.0 cM	A		transglutaminase 2, C polypeptide Curated Ortholog	1	P	1.3	P	0.833	P	J. Biol. Chem.266:479-483 (1991)
?	enzyme	35182_at	2'-5'oligoadenylate synthetase 2, isoform p69		none								-		-		-		-
?	enzyme	35425_at	thioredoxin reductase 1	29	101043_r_at	AV277588	NM_015762	NP_056577	10	A		thioredoxin reductase 1 Curated Ortholog	1.4	A	1.8	A	0.588	A	Gene. 2000 Jan 25;242(1-2):321-30.
?	enzyme	35425_at	thioredoxin reductase 1	30	99885_at	AB027585	NM_015762	NP_056577	10	A		thioredoxin reductase 1 Curated Ortholog	1.2	P	0.809	P	1	P	Gene. 2000 Jan 25;242(1-2):321-30.

Table 42

7	enzyme	39425_at	thioredoxin reductase 1	31	161284_r_at	AV299386	NM_015782	NP_056577	10	A		thioredoxin reductase 1 Curated Ortholog	0.909	P	1.3	P	0.789	P	Gene. 2000 Jan 25;242(1-2):321-30.
7	enzyme	39425_at	thioredoxin reductase 1	32	162642_at	AI854834	NM_015782	NP_056577	10	B		thioredoxin reductase 1 Curated Ortholog	0.323	A	2.8	A	0.586	A	Gene. 2000 Jan 25;242(1-2):321-30.
7	enzyme	40505_at	ubiquitin-conjugating enzyme E2L 6		-	AF159230	NM_019949	NP_064333	2			ubiquitin-conjugating enzyme	-		-		-		Genome Res. 10 (11), 1757-1771 (2000)
7	enzyme	41352_at	sialyltransferase 1 (beta-galactoside abha-2,6-sialytransferase)	33	94431_at	D16106	NM_009175	NP_033201	10 15.5 cM	A		sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) Curated Ortholog	0.385	A	1.3	A	1.8	A	Bioorg. Med. Chem.1;141-145 (1993)
7	enzyme	41352_at	sialyltransferase 1 (beta-galactoside abha-2,6-sialytransferase)	34	167200_r_at	AV024481	NM_009175	NP_033201	10 15.5 cM	C		sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) Curated Ortholog	0.769	A	1.6	A	0.909	A	Bioorg. Med. Chem.1;141-145 (1993)
7	enzyme	41556_s_at	heparan sulfate D-glucosaminyl 3-O-sulfotransferase 1 precursor	35	102410_at	AF019385	NM_010474	NP_034604	5 22.0 cM	A	87.19%	heparan sulfate (glucosamine) 3-O-sulfotransferase 1 Putative Ortholog (highly conserved)	1.4	A	0.4	A	1	P	J. Biol. Chem.272:28008-28019 (1997)

		human		mouse									MASMS						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
8	hypothetical protein	33787_at	KIAA0537 gene product	36	110469_at	AI844322	-	-	10	B	98.27%	ESTs Putative Ortholog (highly conserved)	0.909	A	0.833	A	0.769	A	-
8	hypothetical protein	34714_at	DKFZP564A032 protein	37	109915_at	AA170781	NM_018851	NP_061339	2	B		SAM domain and HD domain, 1 Curated Ortholog	1.2	A	0.303	A	1.1	A	J. Leukoc. Biol. 57:477-483 (1995)
8	hypothetical protein	34714_at	DKFZP564A032 protein	38	103080_at	U15635	NM_018851	NP_061339	2	A		SAM domain and HD domain, 1 Curated Ortholog	1.3	P	1.3	P	0.909	P	J. Leukoc. Biol. 57:477-483 (1995)
8	hypothetical protein	36070_at	cDNA DKFZp586O0118	39	166580_at	AV245197	-	-	-	C	87.81%	RIKEN cDNA 6330404C01 gene Putative Ortholog (highly conserved)	2	A	1	A	0.769	A	-
8	hypothetical protein	38927_at	hypothetical protein, expressed in osteoblast		-	AK020957	-	-	-			RIKEN cDNA B230104P22 gene	-		-		-		Meth. Enzymol. 303, 19-44 (1999)
8	hypothetical protein	37230_at	KIAA0469 gene product		-	BF321302	-	-	-		93.70%	IMAGE:3873822	-		-		-		-
8	hypothetical protein	37784_at	DKFZp564N1116		-	none	-	-	-				-		-		-		-
8	hypothetical protein	41402_at	DKFZP564O0823 protein		-	none	-	-	-				-		-		-		-

		human		mouse									MASMS						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
9	interferon-inducible protein	1107_s_at	interferon-stimulated protein, 15 kDa	40	98822_at	X56602	NM_015783	NP_056598	-	A	84.17%	interferon-stimulated protein (15 kDa) Putative Ortholog (highly conserved)	4.3	P	4.2	P	2.2	P	Unpublished :- 0
9	interferon-inducible protein	38432_at	interferon-stimulated protein, 15 kDa	40	98822_at	X56602	NM_015783	NP_056598	-	A		interferon-stimulated protein (15 kDa) Curated Ortholog	4.3	P	4.2	P	2.2	P	Unpublished :- 0
9	interferon-inducible protein	32814_at	interferon-induced protein with tetratricopeptide repeats 1	41	100981_at	U43084	NM_008331	NP_032357	19	A	65.58%	interferon-induced protein with tetratricopeptide repeats 1 Putative Ortholog	1.8	P	1.9	P	1.6	P	Genomics 24:137-148 (1994)
9	interferon-inducible protein	32814_at	interferon-induced protein with tetratricopeptide repeats 1	42	168289_f_at	AV080198	NM_008331	NP_032357	19	C	65.58%	interferon-induced protein with tetratricopeptide repeats 1 Putative Ortholog	1.3	P	1.1	P	1.2	P	Genomics 24:137-148 (1994)
9	interferon-inducible protein	915_at	interferon-induced protein with tetratricopeptide repeats 1	41	100981_at	U43084	NM_008331	NP_032357	19	A	65.58%	interferon-induced protein with tetratricopeptide repeats 1 Putative Ortholog	1.8	P	1.9	P	1.6	P	Genomics 24:137-148 (1994)

Table 43

9	interferon-inducible protein	916_at	interferon-induced protein with tetratricopeptide repeats 1	42	168299_f_at	AV090188	NM_008331	NP_032357	18	C	85.58%	interferon-induced protein with tetratricopeptide repeats 1 Putative Ortholog	1.3	P	1.1	P	1.2	P	Genomics 24:137-148 (1994)
9	interferon-inducible protein	33304_at	interferon stimulated gene (20kD)	43	103432_at	AW122677	NM_020583	NP_065608	7	A	85.18%	interferon-stimulated protein (20 kDa) Putative Ortholog (highly conserved)	1	P	1.2	P	1	P	Meth. Enzymol. 303:19-44 (1999)
9	interferon-inducible protein	38549_at	viperin (cig5) mRNA	44	109385_at	AI315184	NM_021384	NP_067359	12	B	85.85%	viral hemorrhagic septicemia virus(VHSV) induced gene 1 Putative Ortholog (highly conserved)	0.769	P	1.7	P	0.286	A	J. Virol. 73:1846-1852 (1999)
9	interferon-inducible protein	38584_at	interferon-induced protein with tetratricopeptide repeats 4		none								-		-		-		
9	interferon-inducible protein	40322_at	interleukin 1 receptor-like 1	45	98501_at	Y07519	NM_010743	NP_034873	1 20.0 cM	A	81.93%	interleukin 1 receptor-like 1 Curated Ortholog	0.769		1.8		1		Proc. Natl. Acad. Sci.U.S.A. 86:5708-5712 (1989)
9	interferon-inducible protein	40322_at	interleukin 1 receptor-like 1	46	98500_at	D13695	NM_010743	NP_034873	1 20.0 cM	A	81.75%	interleukin 1 receptor-like 1 Putative Ortholog (highly conserved)	1.3	A	3.4	P	2.4	P	Proc. Natl. Acad. Sci.U.S.A. 86:5708-5712 (1989)
9	interferon-inducible protein	425_at	interferon, alpha-inducible protein 27		none								-		-		-		
9	interferon-inducible protein	464_s_at	interferon-induced protein 35		-	AW986054	-	-	-	-	85.40%	expressed sequence AW986054	-		-		-		-
9	interferon-inducible protein	828_s_at	interferon-induced protein 35		-	AW986054	-	-	-	-	85.40%	expressed sequence AW986054	-		-		-		-
9	interferon-inducible protein	675_at	interferon induced transmembrane protein 1 (9-27)		-	AK003407	-	BAB22771	7F4	-		RIKEN cDNA 1110004C05 gene	-		-		-		Meth. Enzymol. 303, 19-44 (1999)
9	interferon-inducible protein	1358_s_at	interferon, alpha-inducible protein (clone IFI-6-16)		none								-		-		-		
9	interferon-inducible protein	37641_at	hepatitis C-associated microtubular aggregate protein p44, exon 9		none								-		-		-		
9	interferon-inducible protein	39728_at	interferon, gamma-inducible protein 30	47	97444_at	AI844520	NM_023065	NP_075552	8	A	78.22%	interferon gamma inducible protein 30 Putative Ortholog	1.3	A	1.9	A	1.8	A	Science 294:1361-1365 (2001)
9	interferon-inducible protein	39728_at	interferon, gamma-inducible protein 30	48	164423_at	AV076807	NM_023065	NP_075552	8	B	78.22%	interferon gamma inducible protein 30 Putative Ortholog	0.714	A	4	P	4.1	A	Science 294:1361-1365 (2001)
9	interferon-inducible protein	908_at	ISG-54K gene (interferon stimulated gene) encoding a 54 kDA protein	49	164273_at	AV276912	-	-	-	B	86.39%	ESTs Putative Ortholog	1	A	1	A	1.5	A	-

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
10	kinase	1560_g_at	p21 (CDKN1A)-activated kinase 2	50	97823_g_at	AW122689	-	-	16	A	95.19%	DNA segment, Chr 16, ERATO Doi 259, expressed Putative Ortholog	1.1	P	1.1	P	1.1	P	-
10	kinase	1560_g_at	p21 (CDKN1A)-activated kinase 2	51	97822_at	AW122689	-	-	16	A	95.19%	DNA segment, Chr 16, ERATO Doi 259, expressed Putative Ortholog	1	P	0.909	P	0.909	P	-
10	kinase	1560_g_at	p21 (CDKN1A)-activated kinase 2	52	97821_at	AI846058	-	-	16	A	95.19%	DNA segment, Chr 16, ERATO Doi 259, expressed Putative Ortholog	0.909	A	1	P	1	P	-
10	kinase	35985_at	A kinase (PRKA) anchor protein 2	53	101435_at	AF033275	NM_009649	NP_033779	4	A	90.21%	A kinase anchor protein 2 Homolog	0.833	P	0.833	P	1	P	J. Biol. Chem.273:6533-6541 (1998)

Table 44

10	kinase	36632_at	A kinase (PRKA) anchor protein 10	54	163162_at	AI0E0885	NM_018921	NP_084335	11	B		A kinase (PRKA) anchor protein 10 Curated Ortholog	05	A	0.769	A	0.526	A	Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11184-11189 (1997)
10	kinase	38805_s_at	neurotrophic tyrosine kinase, receptor, type 1	55	110116_at	AW124632	-	-	3	B	88.60%	neurotrophic tyrosine kinase, receptor, type 1 Homolog	25	A	12	A	0.909	A	-
10	kinase	38120_at	polycystin 2	58	100951_at	AF014010	NM_008861	NP_032887	5 55.0 cM	A	86.64%	polycystic kidney disease 2 Putative Ortholog (highly conserved)	0.769	P	0.667	P	0.667	P	Genomics 45:220-223 (1997)
10	kinase	38433_at	AXL receptor tyrosine kinase isoform 1,2	57	99136_at	X63535	NM_009488	NP_033491	7 6.0 cM	A	88.68%	AXL receptor tyrosine kinase Putative Ortholog (highly conserved)	0.351	A	0.476	A	0.25	A	Oncogene 6 (10), 1809-1813 (1991)

		human		mouse									MASMS						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
12	membrane protein	1609_g_at	proto-oncogene met, hepatocyte growth factor receptor		-	-	NM_008591	NP_032617	8 4.0 cM	-		met proto-oncogene Putative Ortholog	-		-		-		-
12	membrane protein	1812_s_at	proto-oncogene met, hepatocyte growth factor receptor, alt. transcript 2		-	-	NM_008591	NP_032617	6 4.0 cM	-		met proto-oncogene Putative Ortholog	-		-		-		-
12	membrane protein	35684_at	met proto-oncogene precursor	58	100309_at	Y00871	NM_008591	NP_032617	6 4.0 cM	A	90.17%	met proto-oncogene Putative Ortholog	0.667	A	1	A	1.9	A	Oncogene 2:593-599(1988)
12	membrane protein	31610_at	epithelial protein up-regulated in carcinoma, membrane associate	59	98935_at	AW011791	NM_026018	NP_080294	4	A	83.76%	membrane-associated protein 17 Homolog	1	P	0.909	P	1.1	P	Meth. Enzymol.303:19-44 (1999)
12	membrane protein	31610_at	epithelial protein up-regulated in carcinoma, membrane associate	60	162531_at	AW048375	-	-	-	B	88.35%	BMP and activin membrane-bound inhibitor, homolog (Xenopus laevis)	1	P	0.769	P	0.769	P	-
12	membrane protein	35276_at	claudin 4	61	101410_at	AB000713	NM_009903	NP_034033	5 75.0 cM	A		claudin 4 Curated Ortholog	1.8	A	3.4	A	1	P	J. Biol. Chem. 272 (42), 26652-26658 (1997)
12	membrane protein	36194_at	low density lipoprotein-related protein-associated protein 1(alpha-2-macroglobu	62	100086_at	D00622	-	BAA00500	5	A		low density lipoprotein receptor-related protein associated protein 1 Curated Ortholog	1.1	P	0.714	P	0.833	P	J. Biochem. 108:297-302 (1990)
12	membrane protein	36194_at	low density lipoprotein-related protein-associated protein 1(alpha-2-macroglobu	63	161988_f_at	AV234541	-	-	5	A		low density lipoprotein receptor-related protein associated protein 1 Curated Ortholog	1.3	A	0.714	A	1.1	P	-
12	membrane protein	37168_at	similar to lysosome-associated membrane glycoprotein		none								-		-		-		
12	membrane protein	38995_at	transmembrane protein claudin 5	64	104516_at	U82758	NM_013805	NP_038833	16 11.65 cM	A	87.03%	claudin 5 Putative Ortholog	1.1	P	1.2	P	0.769	P	Lab. Invest. 78:353-363(1998)
12	membrane protein	39081_at	bone marrow stromal cell antigen 2		-	AY013776	NM_033140	NP_444370	18	-	87.60%	protocadherin beta 16 (Pcdhb16)	-		-		-		Cell 97 (6), 779-790 (1999)
12	membrane protein	39695_at	decay accelerating factor for complement (CD55, Cromer blood group system)	65	103817_at	D63679	NM_010016	NP_034146	1 67.6 cM	A		decay accelerating factor 1 Curated Ortholog	1.2	P	1.5	P	1.3	P	J. Immunol. 155:3079-3091(1995)
12	membrane protein	39695_at	decay accelerating factor for complement (CD55, Cromer blood group system)	66	164905_r_at	AY358386	NM_010016	NP_034146	1 67.6 cM	B		decay accelerating factor 1 Curated Ortholog	0.769	A	1	A	1.1	A	J. Immunol. 155:3079-3091(1995)
12	membrane protein	39695_at	decay accelerating factor for complement (CD55, Cromer blood group system)	67	107626_at	AA174516	NM_010016	NP_034146	1 67.6 cM	B		decay accelerating factor 1 Curated Ortholog	1.3	P	1.6	P	1.8	P	J. Immunol. 155:3079-3091(1995)
12	membrane protein	41045_at	secreted and transmembrane 1 precusor	68	115133_at	AI875165	NM_021401, NM_028907	NP_067376, NP_081183	11	B		secreted and transmembrane 1 Curated Ortholog	0435	A	0.5	A	0.625	A	Meth. Enzymol. 303:19-44(1999)

		human		mouse									MASMS						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference

Table 45

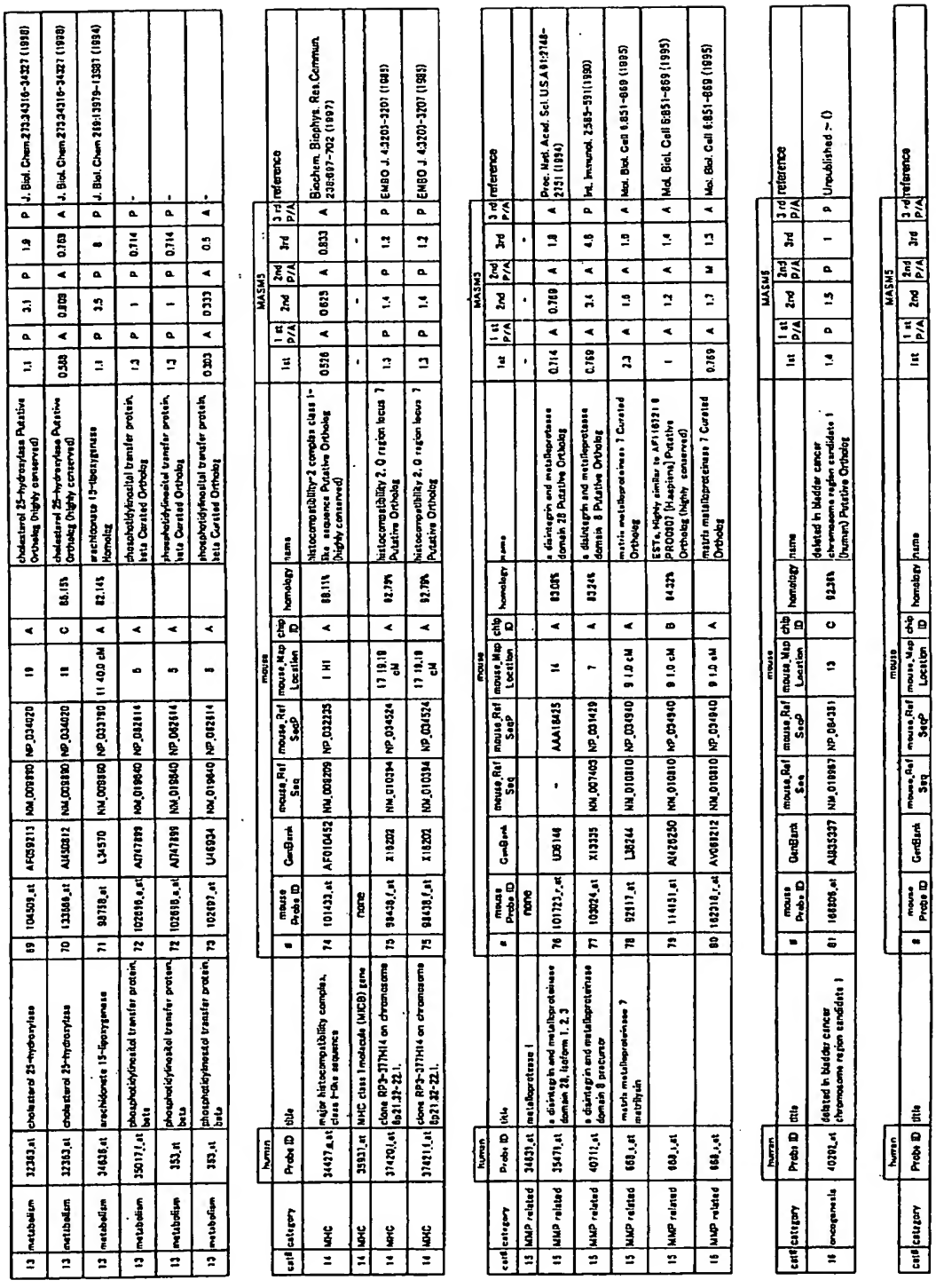


Table 46

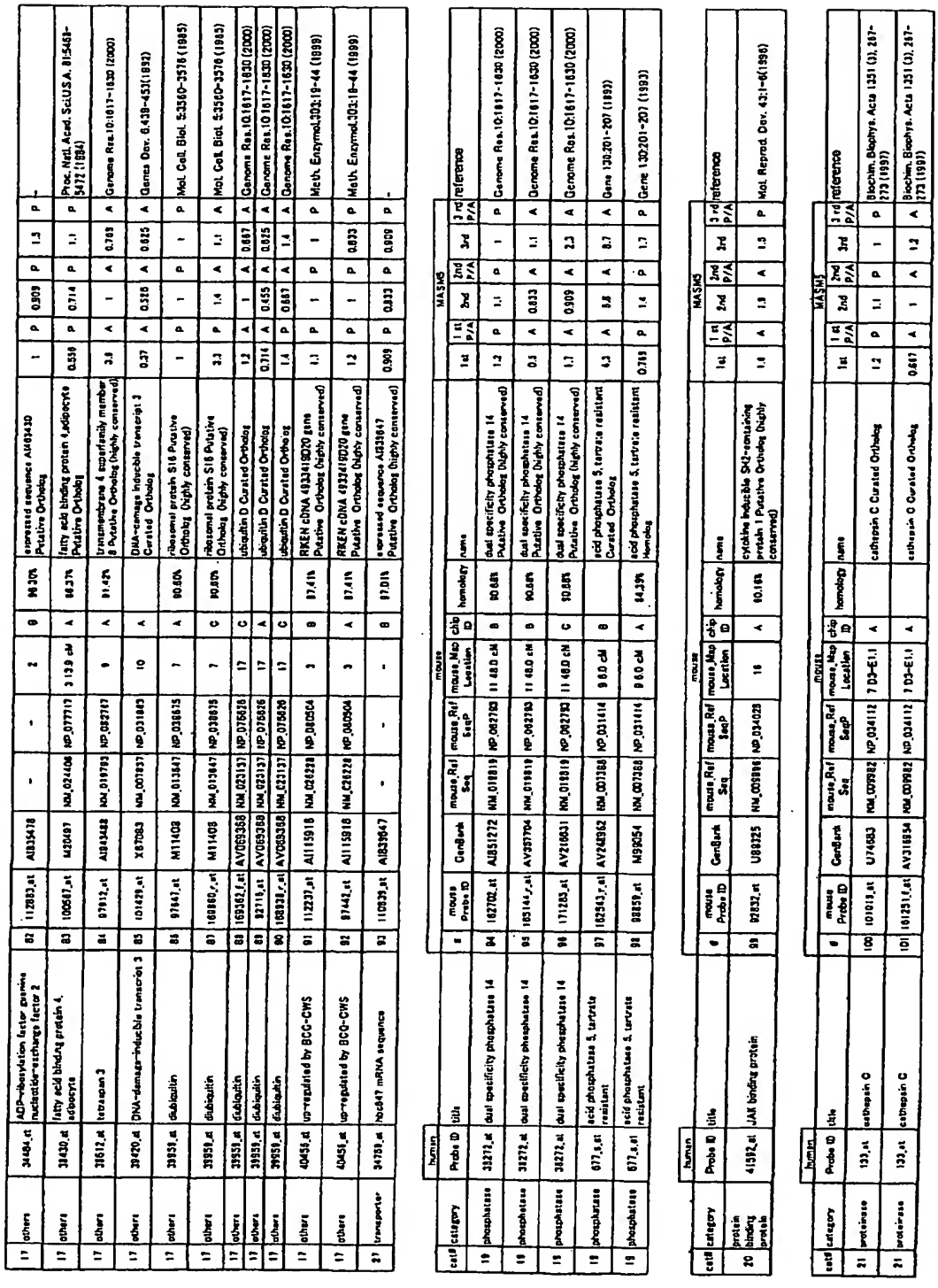


Table 47

cat#	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
21	proteinase	133_at	cathepsin C	102	101020_at	AI842687	NM_009982	NP_034112	7 D3-E1.1	A		cathepsin C Curated Ortholog	1.8	A	0.825	A	0.909	A	Biochim. Biophys. Acta 1351 (3), 267-273 (1997)
21	proteinase	34702_f_at	endogenous retroviral protease		none								-		-		-		
21	proteinase	40491_at	complement component 1, s subcomponent		-	AA798057	-	-	-	-	86.70%	complement component 1, s subcomponent	-		-		-		-
21	proteinase	811_at	ubiquitin fusion degradation 1-like	103	93303_at	U54445	NM_011672	NP_035802	16 11.75 cM	A		ubiquitin fusion degradation 1 like Curated Ortholog	0.667	M	0.303	A	1.3	P	Hum. Mol. Genet.6:259-265 (1997)

cat#	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
22	proteinase inhibitor	1549_s_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4		-	AF063937	NM_009126	NP_033152	1 E1-E2	-	60.00%	squamous cell carcinoma antigen 2	-		-		-		Genomics 54 (2), 297-304 (1998)
22	proteinase inhibitor	32829_at	fetuin B	104	108524_at	U84445	NM_011672	NP_035802	16 11.75 cM	B	85.12%	fetuin beta Putative Ortholog (highly conserved)	1.2	A	0.278	A	0.714	A	Hum. Mol. Genet. 6: 259-265 (1997)
22	proteinase inhibitor	33101_g_at	fetuin B	104	108524_at	U84445	NM_011672	NP_035802	16 11.75 cM	B	85.12%	fetuin beta Putative Ortholog (highly conserved)	1.2	A	0.278	A	0.714	A	Hum. Mol. Genet. 6: 259-265 (1997)
22	proteinase inhibitor	34781_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6	105	96060_at	U25844	NM_009254	NP_033280	13 16.0 cM	A		serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 Curated Ortholog	1.1	P	0.714	P	0.714	P	J. Biol. Chem.270:16089-16096 (1995)
22	proteinase inhibitor	34783_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6	106	113899_at	AW121899	NM_007840	NP_031866	11 63.0 cM	B	100.00%	DEAD (aspartate-glutamate-alanine-aspartate) box polypeptide 5 Putative Ortholog	0.909	P	0.714	P	1.4	P	Life Sci. 52:917-926 (1993)
22	proteinase inhibitor	34789_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6	107	93493_at	X65627	NM_007840	NP_031866	11 63.0 cM	A	100.00%	DEAD (aspartate-glutamate-alanine-aspartate) box polypeptide 5 Putative Ortholog	1	P	1	P	1.1	P	Life Sci. 52:917-926 (1993)
22	proteinase inhibitor	37185_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	108	137166_r_at	AI327311	NM_011111	NP_035241	1 61.1 cM	C	84.17%	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 Curated Ortholog	0.667	A	0.667	A	1.2	A	EMBO J. 8:3287-3294 (1989)
22	proteinase inhibitor	37185_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	109	92978_s_at	X16490	NM_011111	NP_035241	1 61.1 cM	A	84.17%	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 Putative Ortholog (highly conserved)	2.1	P	0.453	P	1.7	A	EMBO J. 8:3287-3294 (1989)

cat#	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
24	signal transduction	32005_at	pro-melanin-concentrating hormone	110	163453_at	AI598769	-	-	-	B	87.54%	RIKEN cDNA A230109K23 gene Putative Ortholog (highly conserved)	1.6	A	1.4	A	1.4	A	-
24	signal transduction	32005_at	pro-melanin-concentrating hormone	111	166475_r_at	AV148333	-	-	-	C	87.54%	RIKEN cDNA A230109K23 gene Putative Ortholog (highly conserved)	1.2	A	0.559	A	0.714	A	-
24	signal transduction	33291_at	RAS guanyl releasing protein 1	112	98307_at	AF106070	NM_011246	NP_035376	2 65.0 cM	A		RAS guanyl releasing protein 1 Curated Ortholog	0.5	A	1.7	M	1.3	A	Unpublished :- ()
24	signal transduction	33291_at	RAS guanyl releasing protein 1	113	167498_i_at	AV313083	NM_011246	NP_035376	2 65.0 cM	C		RAS guanyl releasing protein 1 Curated Ortholog	0.833	A	1.6	A	2.4	A	Unpublished :- ()
24	signal transduction	37014_at	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	114	98417_at	M21038	NM_010846	NP_031978	16 71.2 cM	A		myxovirus (influenza virus) resistance 1 Curated Ortholog	1.1	A	2.2	A	3	A	Cell 44:147-158 (1986)
24	signal transduction	37890_at	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	115	103611_at	AB012693	NM_010581	NP_034711	16	A		integrin-associated protein Curated Ortholog	1	P	1	P	1	P	J. Cell Biol. 123:485-496 (1993)
24	signal transduction	879_at	myxovirus (influenza virus) resistance 2 (mouse)	116	102699_at	J03368	NM_013606	NP_038634	16 71.2 cM	A	89.60%	myxovirus (influenza virus) resistance 2 Putative Ortholog	1.2	A	0.909	P	1.3	A	Mol. Cell. Biol. 8:4524-4528 (1988)

Table 48

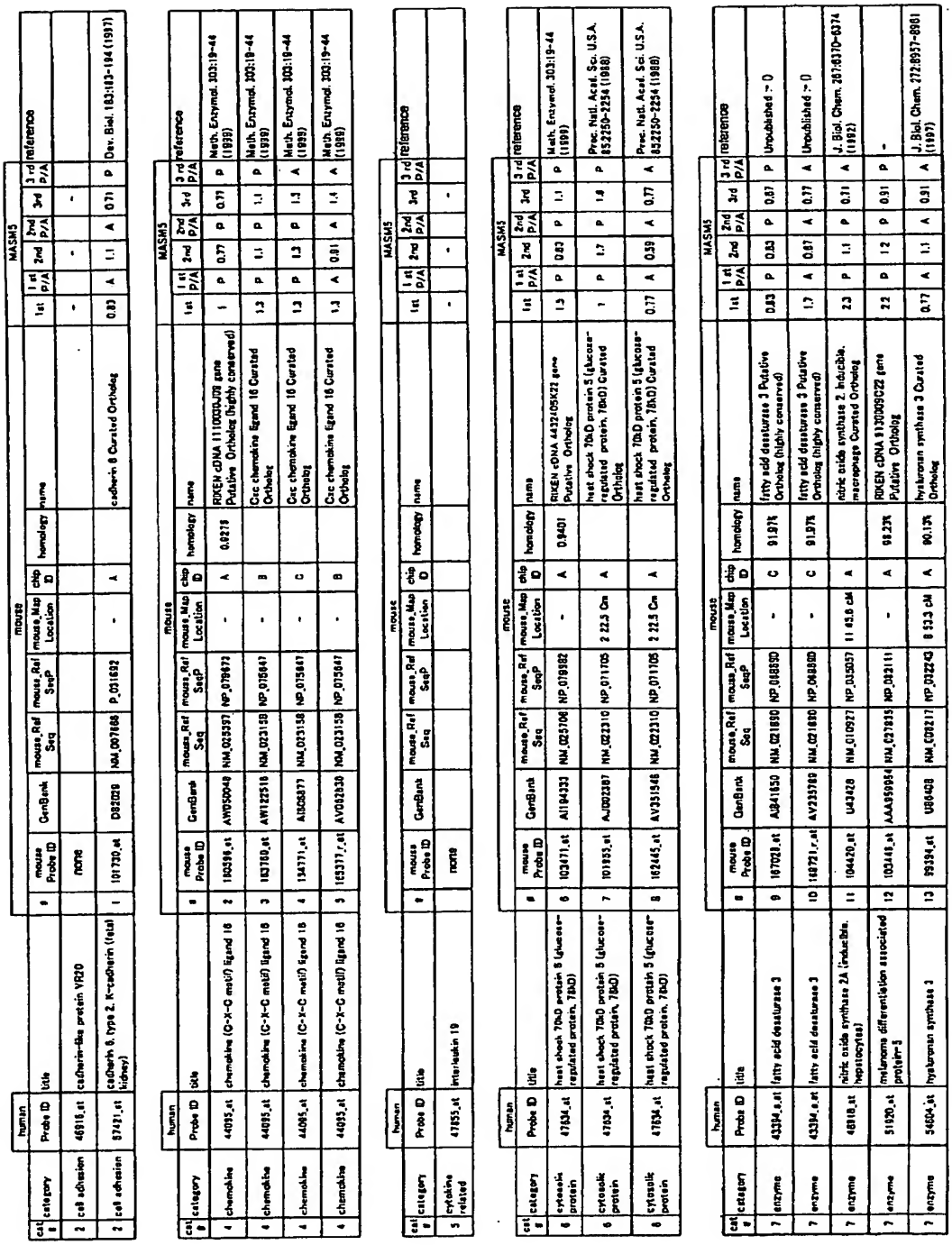
24	signal transduction	875_at	myxovirus (influenza virus) resistance 2 (mouse)	115	98417_at	M21038	NM_010846	NP_034976	16 71.2 cM	A		myxovirus (influenza virus) resistance 1 Curated Ortholog	1.1	A	2.2	A	3	A	Cell 44:147-158 (1986)

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
25	structural protein	39951_at	plastin I		-	AI427122	-	-	-	-	89.30%	expressed sequence AI427122 (AI427122)	-		-		-		-
25	structural protein	601_s_at	keratin type 16 gene, exon 8	117	164428_i_at	AV085754	NM_008470	NP_032496	11 D	B		keratin complex 1, acidic, gene 16 Curated Ortholog	1.5	A	1.6	A	0.625	A	J. Biol. Chem.273:32265-32272 (1998)
25	structural protein	601_s_at	keratin type 16 gene, exon 8	118	103589_at	AF053235	NM_008470	NP_032496	11 D	A		keratin complex 1, acidic, gene 16 Curated Ortholog	1.8	A	1.3	A	1.1	A	J. Biol. Chem.273:32265-32272 (1998)

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
26	transcription factor	32859_at	signal transducer and activator of transcription 1, 91kD	119	101465_at	U06924	NM_009283	NP_033309	1 25.9 cM	A		signal transducer and activator of transcription 1 Curated Ortholog	1.8	P	1.6	P	1	P	Science 264:95-98 (1994)
26	transcription factor	32859_at	signal transducer and activator of transcription 1, 91kD	120	114635_at	AA960121	NM_009283	NP_033309	1 25.9 cM	B		signal transducer and activator of transcription 1 Curated Ortholog	2	P	1.9	P	1.1	P	Science 264:95-98 (1994)
26	transcription factor	32863_g_at	signal transducer and activator of transcription 1, 91kD	119	101465_at	U06924	NM_009283	NP_033309	1 25.9 cM	A		signal transducer and activator of transcription 1 Curated Ortholog	1.8	P	1.6	P	1	P	Science 264:95-98 (1994)
26	transcription factor	32863_g_at	signal transducer and activator of transcription 1, 91kD	120	114635_at	AA960121	NM_009283	NP_033309	1 25.9 cM	B		signal transducer and activator of transcription 1 Curated Ortholog	2	P	1.9	P	1.1	P	Science 264:95-98 (1994)
26	transcription factor	33338_at	STAT1	119	101465_at	U06924	NM_009283	NP_033309	1 25.9 cM	A		signal transducer and activator of transcription 1 Curated Ortholog	1.8	P	1.6	P	1	P	Science 264:95-98 (1994)
26	transcription factor	33339_g_at	STAT1	119	101465_at	U06924	NM_009283	NP_033309	1 25.9 cM	A		signal transducer and activator of transcription 1 Curated Ortholog	1.8	P	1.6	P	1	P	Science 264:95-98 (1994)
26	transcription factor	32941_at	c-myc promoter-binding protein	121	93281_at	AF049125	NM_011992	NP_036122	9	A	80.68%	reticulocalbin 2 Putative Ortholog (highly conserved)	0.909	P	0.833	P	0.909	P	J. Neurochem., 64:2339-2344 (1995)
26	transcription factor	33288_i_at	zinc finger protein 263	122	109154_at	AW121894	-	-	16	B	84.67%	zinc finger protein 263 Putative Ortholog	0.769	P	0.833	P	1.3	P	-
26	transcription factor	35412_at	RNA polymerase B transcriptional regulation mediator (Med6)		-	AK005232	NM_027213	NP_081489	12	-		RIKEN cDNA 1500012F11 gene	-		-		-		Meth. Enzymol. 303, 19-44 (1999)
26	transcription factor	36412_s_at	Interferon regulatory factor 7B mRNA		-	U73037	NM_016850	NP_058546	7 F4	-	78.90%	interferon regulatory factor 7 (Irf7)	-		-		-		Meth. Enzymol. 303, 19-44 (1999)
26	transcription factor	37514_at	nuclear factor, interleukin 3 regulated	123	164758_i_at	AV222514	NM_017373	NP_059069	13 32.0 cM	B	87.50%	nuclear factor, interleukin 3, regulated Curated Ortholog	1.4	A	0.714	A	1.3	A	Proc. Natl. Acad. Sci. U.S.A. 94:2809-2814 (1997)

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
27	transporter	36378_at	pendrin		-	AF167411	NM_011867	NP_035997	12 B1	-		solute carrier family 26, member 4 (Slc26a4)	-		-		-		-
27	transporter	41018_at	neutrophil cytosolic factor 2	126	102326_at	AB002664	NM_010877	NP_035007	1 76.1 cM	A		neutrophil cytosolic factor 2 Curated Ortholog	2	M	2.2	P	1.2	P	Eur. J. Biochem.251:573-582 (1998)

Table 49



cat #	category	human			mouse								MASM5					
		Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
2	cell adhesion	46918_at	cadherin-like protein VR20		none								-		-		-		
2	cell adhesion	37491_at	cadherin 6, type 2, K-cadherin (fetal kidney)	1	101730_at	D83209	NM_007668	P_031692	-	A		cadherin 6 Curated Ortholog	0.83	A	1.1	A	0.71	P	Dev. Biol. 183:103-114 (1997)
4	chemokine	44095_at	chemokine (C-X-C motif) ligand 16	2	160396_s1	AW050048	NM_023397	NP_075872	-	A	0.8218	RIKEN cDNA 1110004J08 gene Putative Ortholog (highly conserved)	1	P	0.77	P	0.77	P	Meth. Enzymol. 303:19-44 (1999)
4	chemokine	44095_at	chemokine (C-X-C motif) ligand 16	3	163760_at	AW122518	NM_023158	NP_075847	-	B		Cxc chemokine ligand 16 Curated Ortholog	1.3	P	1.1	P	1.1	P	Meth. Enzymol. 303:19-44 (1999)
4	chemokine	44095_at	chemokine (C-X-C motif) ligand 16	4	134771_at	AI808877	NM_023158	NP_075847	-	C		Cxc chemokine ligand 16 Curated Ortholog	1.3	P	1.3	P	1.3	A	Meth. Enzymol. 303:19-44 (1999)
4	chemokine	44095_at	chemokine (C-X-C motif) ligand 16	5	163377_r_at	AV042930	NM_023158	NP_075847	-	B		Cxc chemokine ligand 16 Curated Ortholog	1.3	A	0.81	A	1.4	A	Meth. Enzymol. 303:19-44 (1999)
5	cytokine related	47855_at	interleukin 18		none								-		-		-		
6	cytosolic protein	47834_at	heat shock 70kD protein 5 (glucose-regulated protein, 70kD)	6	103471_at	AI194333	NM_025706	NP_079982	-	A	0.9401	RIKEN cDNA 4432405K22 gene Putative Ortholog	1.5	P	0.83	P	1.1	P	Meth. Enzymol. 303:19-44 (1999)
6	cytosolic protein	47834_at	heat shock 70kD protein 5 (glucose-regulated protein, 70kD)	7	101925_at	AJ002387	NM_022310	NP_071705	2 22.5 Cm	A		heat shock 70kD protein 5 (glucose-regulated protein, 70kD) Curated Ortholog	1	P	1.7	P	1.8	P	Proc. Natl. Acad. Sci. U.S.A. 85:2250-2254 (1988)
6	cytosolic protein	47834_at	heat shock 70kD protein 5 (glucose-regulated protein, 70kD)	8	102445_at	AV351348	NM_022310	NP_071705	2 22.5 Cm	A		heat shock 70kD protein 5 (glucose-regulated protein, 70kD) Curated Ortholog	0.77	A	0.59	A	0.77	A	Proc. Natl. Acad. Sci. U.S.A. 85:2250-2254 (1988)
7	enzyme	43394_at	fatty acid desaturase 3	9	167028_at	AJ041650	NM_021890	NP_068590	-	C	91.97%	fatty acid desaturase 3 Putative Ortholog (highly conserved)	0.83	P	0.83	P	0.87	P	Unpublished :- 0
7	enzyme	43394_at	fatty acid desaturase 3	10	168721_r_at	AV235789	NM_021890	NP_068590	-	C	91.97%	fatty acid desaturase 3 Putative Ortholog (highly conserved)	1.7	A	0.87	A	0.77	A	Unpublished :- 0
7	enzyme	48818_at	nitric oxide synthase 2A (inducible, hepatocytes)	11	104420_at	U43428	NM_010927	NP_035057	11 45.0 cM	A		nitric oxide synthase 2, inducible, macrophage Curated Ortholog	2.3	P	1.1	P	0.71	A	J. Biol. Chem. 267:6370-6374 (1992)
7	enzyme	51920_at	melanoma differentiation associated protein-5	12	103448_at	AA459954	NM_021911	NP_068735	-	A	98.23%	RIKEN cDNA 9130009C22 gene Putative Ortholog	2.2	P	1.2	P	0.91	P	-
7	enzyme	54604_at	hyaluronan synthase 3	13	99394_at	U86608	NM_008217	NP_032243	9 33.3 cM	A	90.13%	hyaluronan synthase 3 Curated Ortholog	0.77	A	1.1	A	0.91	A	J. Biol. Chem. 272:8957-8961 (1997)

Table 50

cat #	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homdogy	name	MASNS 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
7	enzyme	57151_at	ADP-ribosylation factor-like 7	14	108048_at	AI836288	-	-	-	B	93.75%	ESTs Homolog	0.77	P	1	P	0.83	P	-
7	enzyme	59215_at	RNA helicase		none														
7	enzyme	51925_at	ESTs, Weakly similar to phosphatidylserine-specific phospholipase A1 deltaC (H.sapiens)	15	110639_at	AW108146	-	-	-	B	84.09%	ESTs, Weakly similar to A34671 triacylglycerol lipase (M.musculus) Putative Ortholog	0.71	A	0.24	A	0.63	A	-
8	hypothetical protein	43366_at	hypothetical protein FLJ10261	16	107112_at	AI121797	-	-	-	B	88.10%	Mus musculus, clone MGC:8241, mRNA, complete cds Putative Ortholog(highly conserved)	1.2	P	1.8	P	1.4	P	-
8	hypothetical protein	43363_at	hypothetical protein FLJ10261	16	107112_at	AI121797	-	-	-	B	88.10%	Mus musculus, clone MGC:8241, mRNA, complete cds Putative Ortholog (highly conserved)	1.2	P	1.8	P	1.4	P	-
8	hypothetical protein	50209_at	hypothetical protein FLJ14281	17	116602_at	AI843057	-	-	-	B	91.34%	RIKEN cDNA 5730496F10 gene Putative Ortholog (highly conserved)	1.4	A	1.5	A	1.4	A	-
8	hypothetical protein	50209_at	hypothetical protein FLJ14281	18	183384_at	AA472475	-	-	-	B	91.34%	RIKEN cDNA 5730496F10 gene Putative Ortholog (highly conserved)	0.77	P	0.77	P	1	P	-
8	hypothetical protein	50209_at	hypothetical protein FLJ14281	19	168478_s_at	AV366163	-	-	-	C	91.34%	RIKEN cDNA 5730496F10 gene Putative Ortholog (highly conserved)	0.91	P	1.1	P	1.3	P	-
8	hypothetical protein	53777_at	hypothetical protein FLJ22693		-	BE687722	-	-	-	-	99.60%	ESTs	-		-		-		-
8	hypothetical protein	56959_at	hypothetical protein FLJ22332		none								-		-		-		
8	hypothetical protein	57197_at	hypothetical protein DKFZp566J091		-	AK020110	NM_028999	NP_084278	-	-		limb-bud and heart (Lbh-pending)	-		-		-		Meth. Enzymol. 303, 19-44 (1999)
8	hypothetical protein	58957_at	hypothetical protein FLJ20637	20	113253_r_at	AI852111	-	-	-	B	89.19%	RIKEN cDNA 2510038N07 gene Putative Ortholog	1.6	P	1.1	A	1.3	A	-
8	hypothetical protein	58957_at	hypothetical protein FLJ20637	21	170481_i_at	AV209883	-	-	-	C	89.19%	RIKEN cDNA 2510038N08 gene Putative Ortholog	2.1	A	0.71	A	1.2	A	-
8	hypothetical protein	58957_at	hypothetical protein FLJ20637	22	115732_at	AI530075	-	-	-	B	89.19%	RIKEN cDNA 2510038N09 gene Putative Ortholog	1.2	A	1.3	A	1.4	A	-
14	MHC	48203_f_at	hypothetical protein DKFZp547I014		none								-		-		-		
8	hypothetical protein	44127_at	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 994846	23	106844_at	AW047110	NM_009370	NP_033396	4 18.3 cM	B	92.73%	transforming growth factor, beta receptor I Homolog	0.91	P	0.77	P	0.77	P	Biochem. Biophys. Res. Commun. 198: 1054-1062 (1994)
8	hypothetical protein	44127_at	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 994846	24	92427_at	D25540	NM_009370	NP_033396	4 18.3 cM	A	92.73%	transforming growth factor, beta receptor I Homolog	2	A	0.38	A	1.2	A	Biochem. Biophys. Res. Commun. 198: 1054-1062 (1994)
8	hypothetical protein	46038_at	Homo sapiens cDNA FLJ31051 fis, clone HSYRA2000605, weakly similar to MYOSIN HEAVY CHAIN, CLONE 203		none														
8	hypothetical protein	47087_at	Homo sapiens cDNA FLJ25117 fis, clone CBR05757		none														
8	hypothetical protein	48826_s_at	Homo sapiens mRNA; cDNA DKFZp434D0818 (from clone DKFZp434D0818)		none								-		-		-		
8	hypothetical protein	52307_at	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 994846	23	106844_at	AW047110	NM_009370	NP_033396	4 18.3 cM	B	92.73%	transforming growth factor, beta receptor I Homolog	0.91	P	0.77	P	0.77	P	Biochem. Biophys. Res. Commun. 198: 1054-1062 (1994)

Table 51

cat #	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
8	hypothetical protein	52307_at	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 994846	24	92427_at	D25540	NM_009370	NP_033396	4 19.3 cM	A	92.73%	transforming growth factor, beta receptor I Homolog	2	A	0.35	A	1.2	A	Biochem. Biophys. Res. Commun. 198: 1054-1062 (1994)
8	hypothetical protein	52327_s_at	Homo sapiens mRNA; cDNA DKFZp434O227 (from clone DKFZp434O227)	25	102907_at	AW125043	-	-	-	A	0.0395	expressed sequence AV253284 Putative Ortholog	1	P	0.83	P	0.83	P	-
8	hypothetical protein	52539_at	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 994846	23	106844_at	AW047110	NM_009370	NP_033399	4 19.3 cM	B	92.73%	transforming growth factor, beta receptor I Homolog	0.91	P	0.77	P	0.77	P	Biochem. Biophys. Res. Commun. 198: 1054-1062 (1994)
8	hypothetical protein	52539_at	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 994846	24	92427_at	D25540	NM_009370	NP_033398	4 19.3 cM	A	92.73%	transforming growth factor, beta receptor I Homolog	2	A	0.35	A	1.2	A	Biochem. Biophys. Res. Commun. 198: 1054-1062 (1994)
8	hypothetical protein	52622_at	Homo sapiens cDNA FLJ11812 fis, clone HEMBA1006364		none							·	-		-		-		....
8	hypothetical protein	53010_at	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2068071	26	114794_at	AA693185	-	-	-	B	90.60%	RIKEN cDNA 2310071E10 gene Putative Ortholog (highly conserved)	1	P	0.48	A	0.83	A	-
8	hypothetical protein	53061_at	Homo sapiens cDNA FLJ21425 fis, clone COL04162		none								-		-		-		
8	hypothetical protein	54033_at	Homo sapiens cDNA FLJ22547 fis, clone HSI00356	27	92971_at	AW125849	-	-	-	A	88.89%	RIKEN cDNA 2210012L08 gene Putative Ortholog (highly conserved)	0.77	A	1.3	A	1.1	P	-
8	hypothetical protein	54885_at	Homo sapiens mRNA; cDNA DKFZp434O227 (from clone DKFZp434O227)	28	102907_at	AW125043	-	-	-	A	93.95%	expressed sequence AV253284 Putative Ortholog	1	P	0.83	P	0.83	P	-
8	hypothetical protein	54897_at	Homo sapiens cDNA FLJ31528 fis, clone NT2RI2002211	29	114119_at	AW124823	-	-	-	B	92.44%	ESTs Putative Ortholog (highly conserved)	1.3	P	1	P	0.71	A	-
8	hypothetical protein	57050_at	KIAA1268 protein	30	112671_at	AW122101	-	-	-	B	83.66%	clone MGC:29390 IMAGE:5065398, mRNA, complete cds Putative Ortholog	1.4	P	1.4	P	1.2	P	-
8	hypothetical protein	59518_at	KIAA1268 protein	30	112671_at	AW122101	-	-	-	B	83.66%	clone MGC:29390 IMAGE:5065398, mRNA, complete cds Putative Ortholog	1.4	P	1.4	P	1.2	P	-
8	hypothetical protein	57694_at	Homo sapiens cDNA FLJ22629 fis, clone HSI06179		none														
8	hypothetical protein	57698_at	Homo sapiens cDNA FLJ22629 fis, clone HSI06180		none														
8	hypothetical protein	59038_at	Homo sapiens cDNA FLJ14241 fis, clone OVARC1000533		none														

cat #	category	human Probe ID	title	#	mouse Probe ID	mouse GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
9	interferon-inducible protein	48864_at	interferon, alpha-inducible protein 27		none								-		-		-		
9	interferon-inducible protein	52815_at	guanylate binding protein 5	31	95974_at	M55544	NM_010259	NP_034389	3 67.4 cM	A	91.89%	guanylate nucleotide binding protein 1 Putative Ortholog	2.9	P	1.8	P	1.1	P	Mol. Cell. Biol. 11:4717-4725 (1991)

cat #	category	human Probe ID	title	#	mouse Probe ID	mouse GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
10	kinase	48035_at	A kinase (PRKA) anchor protein 2	32	101435_at	AF033275	NM_009649	NP_033779	-	A	92.21%	A kinase anchor protein 2 Homolog	0.83	P	0.83	P	1	P	J. Biol. Chem. 273:6533-6541 (1998)
10	kinase	51085_at	CamKI-like protein kinase		AA060013	-	-	-	-		91.40%	ESTs							-

Table 52

10	kinase	51923_at	sphingosine kinase 1	33	103839_at	AF064748	NM_011451	NP_035581	-	A	97.32%	sphingosine kinase 1 Putative Ortholog (highly conserved)	0.42	A	0.42	A	0.77	A	J. Biol. Chem. 273 (37), 23722-23728 (1998)
10	kinase	51923_at	sphingosine kinase 1	34	164777_i_at	AV250528	NM_011451	NP_035581	-	B	97.32%	sphingosine kinase 1 Putative Ortholog (highly conserved)	2.2	A	0.4	A	1.3	A	J. Biol. Chem. 273 (37), 23722-23728 (1998)
10	kinase	56474_at	protein kinase H11	35	162448_f_at	AV354094	NM_030704	NP_109629	5 59.0 cM	A	90.48%	crystallin, alpha C Putative Ortholog (highly conserved)	0.35	A	0.35	A	0.77	A	Meth. Enzymol. 303:19-44 (1999)
10	kinase	56474_at	protein kinase H11	36	160139_at	AI848798	NM_030704	NP_109629	5 59.0 cM	A	90.48%	crystallin, alpha C Putative Ortholog (highly conserved)	0.6	P	3.83	P	0.91	P	Meth. Enzymol. 303:19-44 (1999)

		human		mouse									MASM5						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
12	membrane protein	46260_at	claudin 1	37	160415_at	AI504314	NM_016674	NP_057883	-	A	92.66%	claudin 1 Putative Ortholog (highly conserved)	1.1		1.6		1.4		J. Cell Biol. 141:1539-1550 (1998)
12	membrane protein	46260_at	claudin 1	38	97546_at	AF072127	NM_016674	NP_057883	-	A	92.66%	claudin 1 Putative Ortholog (highly conserved)	1.1		0.53		1.2		J. Cell Biol. 141:1539-1550 (1998)
12	membrane protein	50320_g_at	poliovirus receptor-related 2 (herpesvirus entry mediator B)	39	99934_at	M80206	NM_008990	NP_033016	7 9.0 cM	A		poliovirus sensitivity Curated Ortholog	1	P	0.77	P	0.71	P	J. Virol. 66:2807-2813 (1992)
12	membrane protein	50320_g_at	poliovirus receptor-related 2 (herpesvirus entry mediator B)	40	164850_f_at	AV369774	NM_008990	NP_033016	7 9.0 cM	B		poliovirus sensitivity Curated Ortholog	1.5	A	3.1	A	3.1	A	J. Virol. 66:2807-2813 (1992)
12	membrane protein	50320_g_at	poliovirus receptor-related 2 (herpesvirus entry mediator B)	41	99933_at	D26107	NM_008990	NP_033016	7 9.0 cM	A		poliovirus sensitivity Curated Ortholog	1	P	1.2	P	1.1	P	J. Virol. 66:2807-2813 (1992)
12	membrane protein	51628_at	extracellular glycoprotein EMILIN-2 precursor	42	103811_at	AA981032	-	-	-	B	91.18%	ESTs, Moderately similar to extracellular glycoprotein EMILIN-2 precursor Putative Ortholog (highly conserved)	1	A	1.3	P	1.1	P	-
12	membrane protein	51628_at	extracellular glycoprotein EMILIN-2 precursor	43	170500_at	AV223427	-	-	-	C	91.18%	ESTs, Moderately similar to extracellular glycoprotein EMILIN-2 precursor Putative Ortholog (highly conserved)	2	A	0.48	A	0.91	A	-

		human		mouse									MASM5						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
16	oncogenesis	50388_at	malignant fibrous histiocytoma amplified sequence 1	44	163337_at	AA727483	-	-	-	B	92.68%	ESTs, Highly similar to MASL1 [H.sapiens] Putative Ortholog	0.77	P	1.1	P	1.1	P	-
16	oncogenesis	52167_at	B aggressive lymphoma gene	45	109021_at	AW214142	NM_030253	NP_084529	-	B	87.70%	hypothetical protein, MGC: 7868 Putative Ortholog (highly conserved)	1.4	P	1.6	P	1.1	P	Unpublished - 0

		human		mouse									MASM5						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
17	others	44583_at	SAM domain and HD domain, 1	46	109915_at	AA170781	NM_018851	NP_061339	-	B		SAM domain and HD domain, 1	1.2	A	0.3	A	1.1	A	J. Leukoc. Biol. 57:477-483 (1995)
17	others	44583_at	SAM domain and HD domain, 1	47	103080_at	U15636	NM_018851	NP_061339	-	A		SAM domain and HD domain, 1	1.3	P	1.3	P	0.91	P	J. Leukoc. Biol. 57:477-483 (1995)
17	others	46278_at	chromosome 16 open reading frame 5		AW742692	-	-	-	-		87.50%	expressed sequence AW742692	-		-		-		-
17	others	48358_at	CGI-141 protein	48	166458_at	AI431004	NM_025872	NP_080148	-	C	95.04%	RIKEN cDNA 2310061A22 gene Homolog	0.4	A	3.5	A	0.83	A	Meth. Enzymol. 303:19-44 (1999)

Table 53

17	others	48368_at	CGI-141 protein	49	107908_at	AI016570	NM_025372	NP_080148	-	B	95.04%	RIKEN cDNA 2310081A22 gene Homolog	0.83	A	1.2	A	0.59	A	Meth. Enzymol. 303:19-44 (1999)
17	others	50094_at	serum deprivation response (phosphatidylserine-binding protein)	50	165304_at	AV245062	NM_138741	NP_620080	-	B	91.41%	ESTs, Weakly similar to polymerase I-transcript release factor [M.musculus] Putative Ortholog (highly conserved)	1.8	A	1.2	A	1.3	A	Cell Growth Differ. 4:753-760 (1993)
17	others	50094_at	serum deprivation response (phosphatidylserine-binding protein)	51	160373_i_at	AI839175	NM_138741	NP_620080	-	A	91.41%	ESTs, Weakly similar to polymerase I-transcript release factor [M.musculus] Putative Ortholog (highly conserved)	1	P	0.67	P	0.63	P	Cell Growth Differ. 4:753-760 (1993)
17	others	50398_at	chromosome 12 open reading frame 5	52	111260_at	AI843809	-	-	-	B	82.03%	ESTs, Weakly similar to S67185 hypothetical protein YOR283w - yeast (Saccharomyces cerevisiae) [S.cerevisiae] Putative Ortholog	1.9	A	1.9	A	1.5	A	-
17	others	50398_at	chromosome 12 open reading frame 5	53	166340_at	AA793651	-	-	-	C	82.03%	ESTs, Weakly similar to S67185 hypothetical protein YOR283w - yeast (Saccharomyces cerevisiae) [S.cerevisiae] Putative Ortholog	0.33	A	1.6	A	0.4	A	-
17	others	51238_at	NEDD8 ultimate buster-1	54	165319_at	AV270997	NM_016736	NP_058018	-	B	93.27%	RIKEN cDNA 4931404D21 gene Putative Ortholog	2.4	A	1	A	0.91	A	-
17	others	59657_at	chromosome 21 open reading frame 11	55	168781_at	AV258801	NM_020622	NP_065647	-	C	82.50%	RIKEN cDNA 9030624C24 gene Putative Ortholog	0.44	A	0.91	A	0.91	P	Genomics 78 (1-2), 46-54 (2001)
17	others	59657_at	chromosome 21 open reading frame 11	56	161580_f_at	AV314820	NM_016736	NP_058018	-	A		NY-REN-18 antigen Curated Ortholog	0.91	A	0.53	A	0.91	A	Genome Res. 10:1617-1630 (2000)
17	others	59657_at	chromosome 21 open reading frame 11	57	100570_at	U27462	NM_016736	NP_058018	-	A		NY-REN-18 antigen Curated Ortholog	0.77	P	0.83	P	0.91	P	Genome Res. 10:1617-1630 (2000)
17	others	62878_at	similar to junction-mediating and regulatory protein p300 JMY		none								-		-		-		

		human		mouse									MASMS						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
18	P450	47627_at	cytochrome P450, subfamily IIS, polypeptide 1	58	104550_at	AW123273	NM_028775	NP_083051		A	87.01%	RIKEN cDNA 1200011C15 gene Putative Ortholog	0.91	P	0.71	P	1	P	Meth. Enzymol. 303, 19-44 (1999)

		human		mouse									MASMS						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
20	protein binding protein	48838_s_at	JAK binding protein	59	92832_at	U88325	NM_009896	NP_034026	-	A	90.16%	cytokine inducible SH2-containing protein 1 Curated Ortholog	1.6	A	1.9	A	1.5	P	Mol. Reprod. Dev. 43:1-6 (1996)
20	protein binding protein	47500_i_at	c-myc promoter-binding protein	60	93291_at	AF049125	NM_011992	NP_036122	-	A	80.68	reticulocalbin 2 Putative Ortholog	0.91	P	0.83	P	0.91	P	J. Neurochem. 64:2339-2344 (1995)

		human		mouse									MASMS						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
21	proteinase	51972_at	ubiquitin specific protease 18	61	95024_at	AW047653	NM_011909	NP_036039	6 68.0 cM	A	87.86%	ubiquitin specific protease 18 Putative Ortholog	1.3	P	2.9	P	0.77	P	Mol. Cell. Biol. 19:3029-3038 (1999)

		human		mouse									MASMS						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference

Table 54

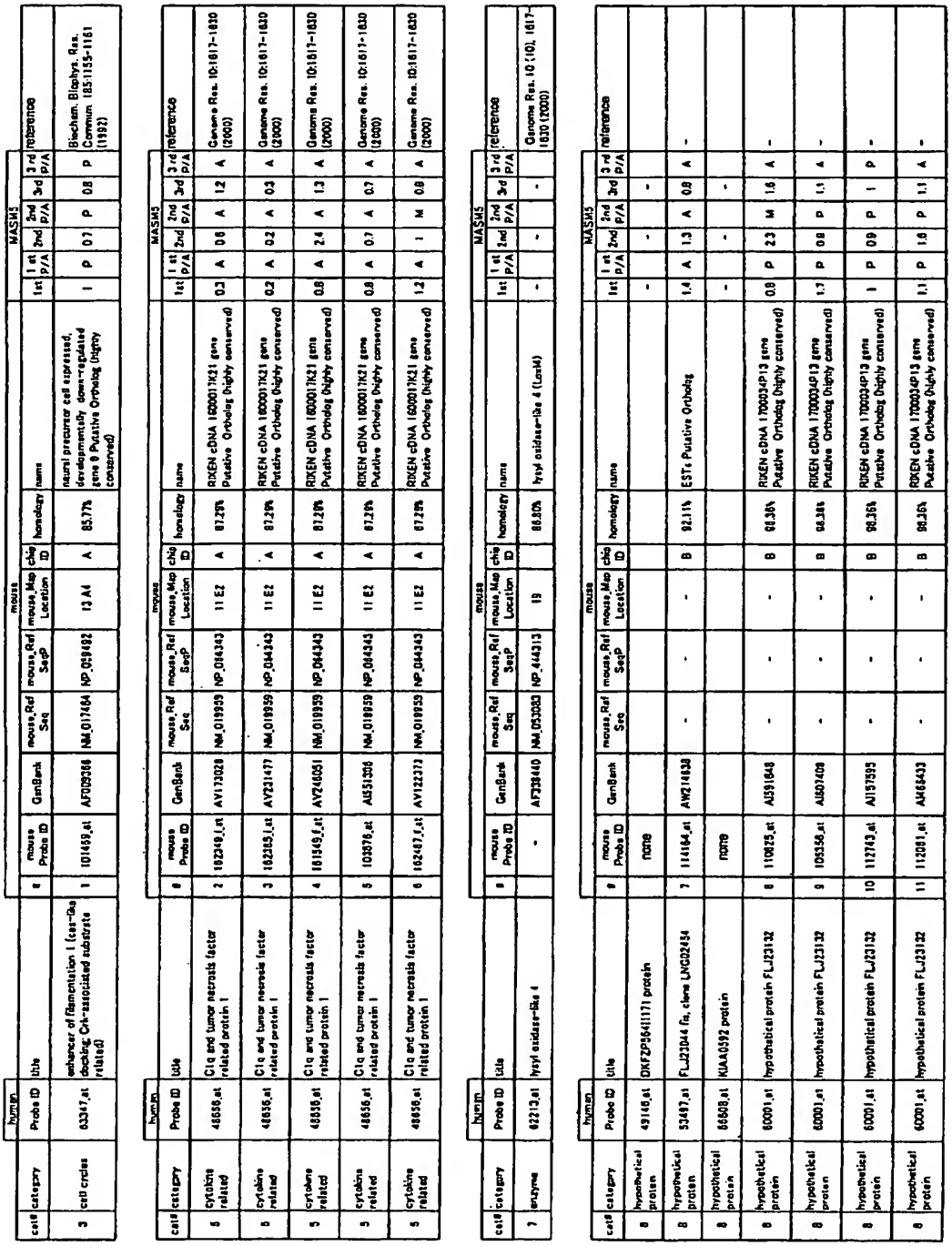
24	signal transduction	55059_at	cytokine inducible SH2-containing protein	62	162383_r_at	AV248532	NM_009895	NP_034025	9 59.0 cM	A	87.36%	cytokine inducible SH2-containing protein Curated Ortholog	0.24	A	1.7	A	0.12	A	EMBO J. 14:2816-2826 (1995)
24	signal transduction	55059_at	cytokine inducible SH2-containing protein	63	100022_at	D89613	NM_009895	NP_034025	9 59.0 cM	A	87.36%	cytokine inducible SH2-containing protein Curated Ortholog	1.2	P	1.6	P	1.5	P	EMBO J. 14:2816-2826 (1995)
24	signal transduction	55107_at	EH-domain containing 3	64	115398_at	AW212283	NM_020578	NP_065603	-	B	90.91%	EH-domain containing 3 Homolog	0.23	A	0.48	A	0.77	A	Unpublished :- ()
24	signal transduction	59759_I_at	4-1BB-mediated signaling molecule	65	163326_i_at	AI816268	NM_027178	NP_081454	-	B	88.42%	RIKEN cDNA 2410005L11 gene Homolog	1.1	A	1.3	A	0.71	A	Meth Enzymol. 333, 19-44 (1999)

		human		mouse									MASM5						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
25	structural protein	48184_at	type I intermediate filament cytokeratin	66	163157_at	AI606261	NM_033373	NP_203537	-	B		type I intermediate filament cytokeratin Curated Ortholog	1.5	P	0.77	P	1.4	P	Unpublished :- ()

		human		mouse									MASM5						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
26	transcription factor	43350_f_at	interferon regulatory factor 7		-	-	NM_016850	NP_058546	7 F4	-	79.90%	interferon regulatory factor 7	-		-		-		Meth. Enzymol. 303, 19-44 (1999)
26	transcription factor	48587_at	Kruppel-like factor 4 (gut)	67	161185_i_at	AV235938	NM_010637	NP_034767	4 19.7 cM	A	89.29%	Kruppel-like factor 4 (gut) Putative Ortholog (highly conserved)	0.77	A	1.5	A	1	A	J. Biol. Chem. 271:9-20017 (2000)
26	transcription factor	48587_at	Kruppel-like factor 4 (gut)	68	99622_at	U20344	NM_010637	NP_034767	4 19.7 cM	A	89.29%	Kruppel-like factor 4 (gut) Putative Ortholog (highly conserved)	1	P	0.83	P	0.77	P	J. Biol. Chem. 271:9-20017 (2000)

		human		mouse									MASM5						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
		42302_at	ESTs		none								-		-		-		
		42721_at	ESTs		none								-		-		-		
		43438_at	wd83d12.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2338199		none								-		-		-		
		45808_at	ESTs	69	161081_at	AA733664	-	-	-	A	99.37%	ESTs Putative Ortholog (highly conserved)	0.83	P	0.83	P	1.2	P	-
		46120_at	ESTs		none								-		-		-		
		46378_at	ESTs		none								-		-		-		
		47252_at	Homo sapiens cDNA, 3' end		none								-		-		-		
		47390_at	ESTs		none								-		-		-		
		51024_at	ESTs		none								-		-		-		
		54922_at	ESTs	70	95020_at	AI848818	-	-	-	A	93.72%	RIKEN cDNA 9130415E20 gene Putative Ortholog (highly conserved)	0.91	P	0.91	P	0.83	P	-
		55491_at	ESTs		none								-		-		-		

Table 55



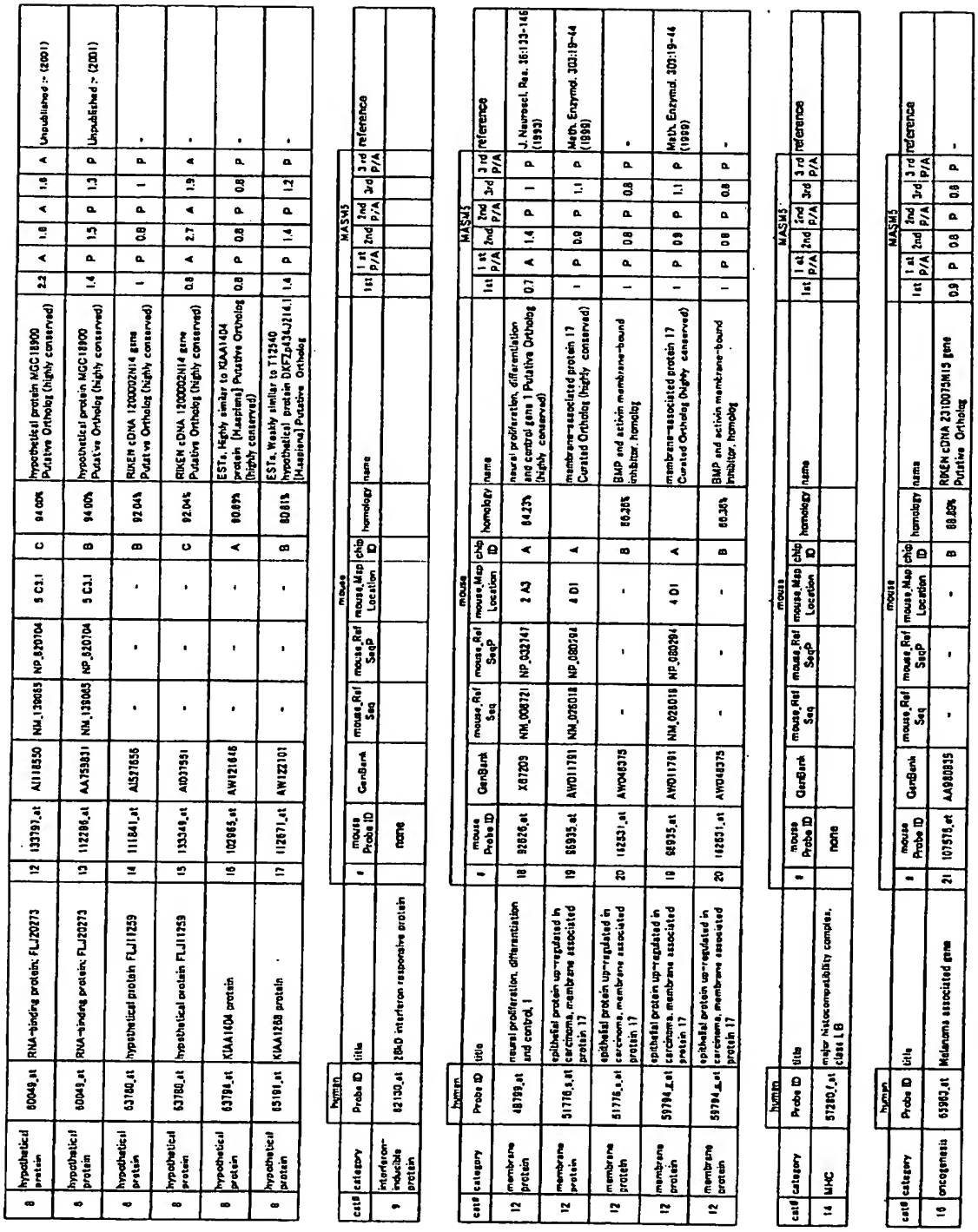
human			mouse						MAS#5			
cell category	Probe ID	title	#	mouse Probe ID	GenBank	mouse,Ref Seq	mouse,Ref SeqP	mouse,Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	3rd reference
3	cell cycles	63347_at	enhancer of filamentation 1 (cas-like docking Crk-associated substrate related)	1	101469_at	AF029386	NM_017484	NP_059482	13 A4	A	85.77%	neural precursor cell expressed, developmentally down-regulated gene 8 Putative Ortholog (highly conserved)	1	P	0.7	P	0.8	P	Biochem. Biophys. Res. Commun. 185:1155-1161 (1992)

human			mouse						MAS#5								
cell category	Probe ID	title	#	mouse Probe ID	GenBank	mouse,Ref Seq	mouse,Ref SeqP	mouse,Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	3rd reference
5	cytokine related	48658_at	C1q and tumor necrosis factor related protein 1	2	102249_i_at	AV113028	NM_019959	NP_064343	11 E2	A	87.29%	RIKEN cDNA 1600017K21 gene Putative Ortholog (highly conserved)	0.3	A	0.6	A	1.2	A	Genome Res. 10:1617-1630 (2000)
5	cytokine related	48658_at	C1q and tumor necrosis factor related protein 1	3	102250_i_at	AV231477	NM_019959	NP_064343	11 E2	A	87.29%	RIKEN cDNA 1600017K21 gene Putative Ortholog (highly conserved)	0.2	A	0.2	A	0.3	A	Genome Res. 10:1617-1630 (2000)
5	cytokine related	48658_at	C1q and tumor necrosis factor related protein 1	4	101549_f_at	AV240051	NM_019959	NP_064343	11 E2	A	87.29%	RIKEN cDNA 1600017K21 gene Putative Ortholog (highly conserved)	0.8	A	2.4	A	1.3	A	Genome Res. 10:1617-1630 (2000)
5	cytokine related	48658_at	C1q and tumor necrosis factor related protein 1	5	103876_at	AI531308	NM_019959	NP_064343	11 E2	A	87.29%	RIKEN cDNA 1600017K21 gene Putative Ortholog (highly conserved)	0.8	A	0.7	A	0.7	A	Genome Res. 10:1617-1630 (2000)
5	cytokine related	48658_at	C1q and tumor necrosis factor related protein 1	6	102497_f_at	AV122372	NM_019959	NP_064343	11 E2	A	87.29%	RIKEN cDNA 1600017K21 gene Putative Ortholog (highly conserved)	1.2	A	1	M	0.8	A	Genome Res. 10:1617-1630 (2000)

human			mouse						MAS#5								
cell category	Probe ID	title	#	mouse Probe ID	GenBank	mouse,Ref Seq	mouse,Ref SeqP	mouse,Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	3rd reference
7	enzyme	62213_at	hyryl oxidase-like 4	-	AF238440	NM_053083	NP_444313	19		86.80%	hyryl oxidase-like 4 (Loxl4)	-		-		-		Genome Res. 10:1610, 1617-1630 (2000)

human			mouse						MAS#5								
cell category	Probe ID	title	#	mouse Probe ID	GenBank	mouse,Ref Seq	mouse,Ref SeqP	mouse,Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	3rd reference
8	hypothetical protein	49148_at	DKFZP564I1171 protein		none							-		-		-		
8	hypothetical protein	53487_at	FLJ23044 fis, clone LNG02434	7	114164_at	AW214838	-	-	-	B	92.11%	ESTs, Putative Ortholog	1.4	A	1.3	A	0.8	A	-
8	hypothetical protein	86808_at	KIAA0592 protein		none							-		-		-		
8	hypothetical protein	60001_at	hypothetical protein FLJ23132	8	110825_at	AI591648	-	-	-	B	98.36%	RIKEN cDNA 1700034P13 gene Putative Ortholog (highly conserved)	0.8	P	2.3	M	1.6	A	-
8	hypothetical protein	60001_at	hypothetical protein FLJ23132	9	105356_at	AI607409	-	-	-	B	98.36%	RIKEN cDNA 1700034P13 gene Putative Ortholog (highly conserved)	1.7	P	0.8	P	1.1	A	-
8	hypothetical protein	60001_at	hypothetical protein FLJ23132	10	112743_at	AI157595	-	-	-	B	98.36%	RIKEN cDNA 1700034P13 gene Putative Ortholog (highly conserved)	1	P	0.9	P	1	P	-
8	hypothetical protein	60001_at	hypothetical protein FLJ23132	11	112081_at	AW656433	-	-	-	B	98.36%	RIKEN cDNA 1700034P13 gene Putative Ortholog (highly conserved)	1.1	P	1.8	P	1.1	A	-

Table 56



8	hypothetical protein	60048_at	RNA-binding protein; FLJ20273	12	133797_at	AI118350	NM_139033	NP_620704	5 C3.1	C	94.00%	hypothetical protein MGC18900 Putative Ortholog (highly conserved)	2.2	A	1.8	A	1.6	A	Unpublished :- (2001)
8	hypothetical protein	60041_at	RNA-binding protein; FLJ20273	13	112286_at	AA753831	NM_139045	NP_620704	5 C3.1	B	94.00%	hypothetical protein MGC18900 Putative Ortholog (highly conserved)	1.4	P	1.5	P	1.3	P	Unpublished :- (2001)
8	hypothetical protein	63780_at	hypothetical protein FLJ11259	14	111841_at	AI537655	-	-	-	B	92.04%	RIKEN cDNA 1200002N14 gene Putative Ortholog (highly conserved)	1	P	0.8	P	1	P	-
8	hypothetical protein	63780_at	hypothetical protein FLJ11259	15	133548_at	AI037951	-	-	-	C	92.04%	RIKEN cDNA 1200002N14 gene Putative Ortholog (highly conserved)	0.8	A	2.7	A	1.9	A	-
8	hypothetical protein	63784_at	KIAA1404 protein	16	102985_at	AW121648	-	-	-	A	80.89%	EST6, Highly similar to KIAA1404 protein [Homo sapiens] Putative Ortholog (highly conserved)	0.8	P	0.8	P	0.8	P	-
8	hypothetical protein	65191_at	KIAA1268 protein	17	112671_at	AW122101	-	-	-	B	80.81%	EST6, Weakly similar to T12540 hypothetical protein DKFZp434J214.1 [Homo sapiens] Putative Ortholog	1.4	P	1.4	P	1.2	P	-

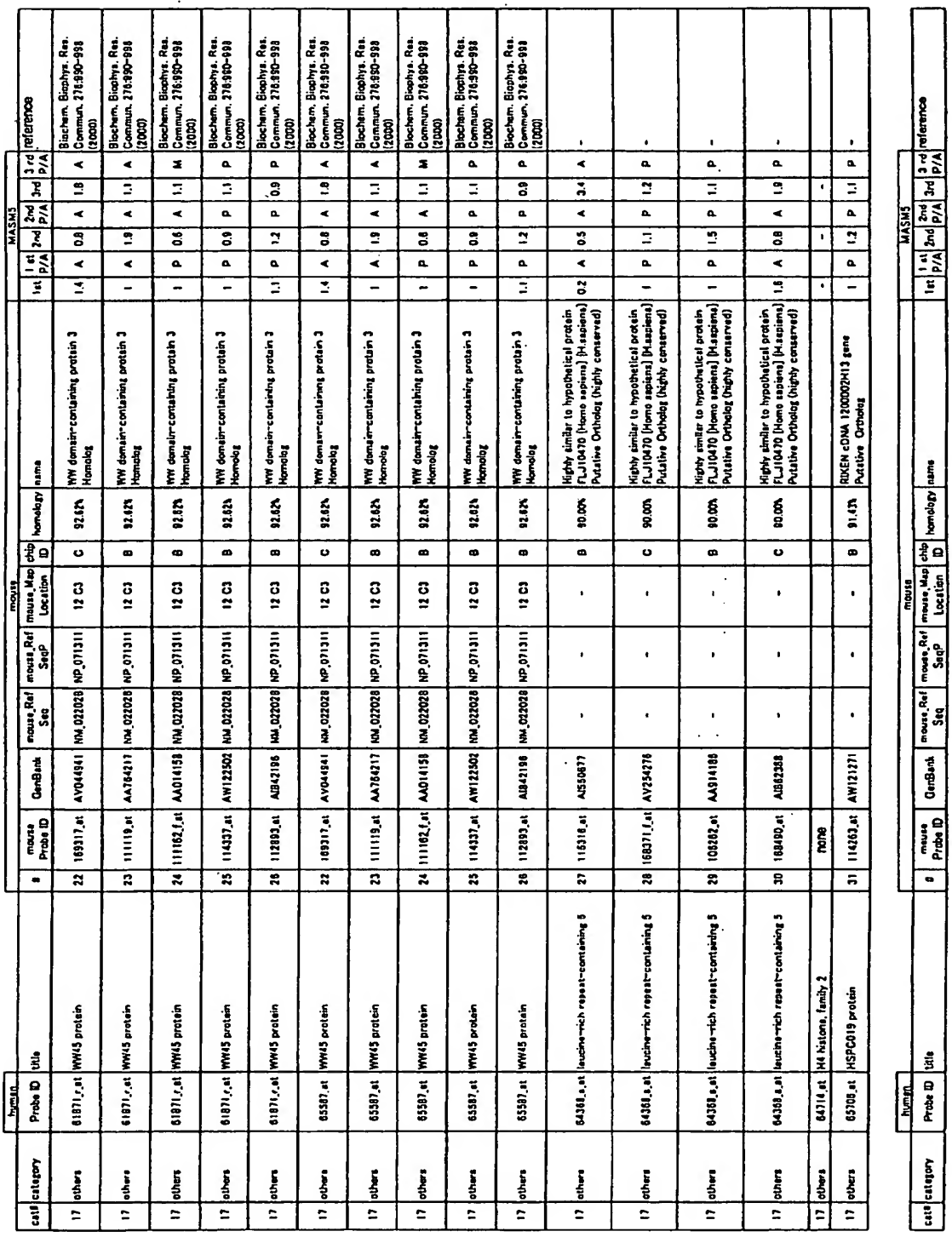
cat#	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5 1st	1 st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
9	interferon-inducible protein	62130_at	18-D interferon responsive protein		none														

cat#	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5 1st	1 st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
12	membrane protein	48799_at	neural proliferation, differentiation and control, 1	18	92828_at	X87209	NM_008721	NP_032747	2 A3	A	84.23%	neural proliferation, differentiation and control gene 1 Putative Ortholog (highly conserved)	0.7	A	1.4	P	1	P	J. Neurosci. Res. 16:133-145 (1993)
12	membrane protein	51778_s_at	epithelial protein up-regulated in carcinoma, membrane associated protein 17	19	86935_at	AW011781	NM_026018	NP_080294	4 D1	A		membrane-associated protein 17 Curated Ortholog (highly conserved)	1	P	0.9	P	1.1	P	Meth. Enzymol. 303:19-44 (1999)
12	membrane protein	51778_s_at	epithelial protein up-regulated in carcinoma, membrane associated protein 17	20	142631_at	AW046375	-	-	-	B	80.36%	BMP and activin membrane-bound inhibitor, homolog	1	P	0.8	P	0.8	P	-
12	membrane protein	59784_at	epithelial protein up-regulated in carcinoma, membrane associated protein 17	19	86935_at	AW011781	NM_026018	NP_080294	4 D1	A		membrane-associated protein 17 Curated Ortholog (highly conserved)	1	P	0.9	P	1.1	P	Meth. Enzymol. 303:19-44 (1999)
12	membrane protein	59784_at	epithelial protein up-regulated in carcinoma, membrane associated protein 17	20	142631_at	AW046375	-	-	-	B	80.36%	BMP and activin membrane-bound inhibitor, homolog	1	P	0.8	P	0.8	P	-

cat#	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5 1st	1 st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
14	MHC	57180_at	major histocompatibility complex, class I B		none														

cat#	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5 1st	1 st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
16	oncogenesis	65963_at	Melanoma associated gene	21	107576_at	AA980815	-	-	-	B	88.82%	RIKEN cDNA 2310075M15 gene Putative Ortholog	0.9	P	0.8	P	0.8	P	-

Table 57



cate	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5 1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
17	others	61871_r_at	WW45 protein	22	169317_at	AV044841	NM_022028	NP_071311	12 C3	C	92.82%	WW domain-containing protein 3 Homolog	1.4	A	0.8	A	1.8	A	Biochem. Biophys. Res. Commun. 276:990-998 (2000)
17	others	61871_r_at	WW45 protein	23	111119_at	AA764217	NM_022028	NP_071311	12 C3	B	92.82%	WW domain-containing protein 3 Homolog	1	A	1.9	A	1.1	A	Biochem. Biophys. Res. Commun. 276:990-998 (2000)
17	others	61871_r_at	WW45 protein	24	111162_f_at	AA014158	NM_022028	NP_071311	12 C3	B	92.82%	WW domain-containing protein 3 Homolog	1	P	0.6	A	1.1	M	Biochem. Biophys. Res. Commun. 276:990-998 (2000)
17	others	61871_r_at	WW45 protein	25	114337_at	AW122502	NM_022028	NP_071311	12 C3	B	92.82%	WW domain-containing protein 3 Homolog	1	P	0.9	P	1.1	P	Biochem. Biophys. Res. Commun. 276:990-998 (2000)
17	others	61871_r_at	WW45 protein	26	112893_at	AI842198	NM_022028	NP_071311	12 C3	B	92.82%	WW domain-containing protein 3 Homolog	1.1	P	1.2	P	0.9	P	Biochem. Biophys. Res. Commun. 276:990-998 (2000)
17	others	65587_at	WW45 protein	22	169317_at	AV044841	NM_022028	NP_071311	12 C3	C	92.82%	WW domain-containing protein 3 Homolog	1.4	A	0.8	A	1.8	A	Biochem. Biophys. Res. Commun. 276:990-998 (2000)
17	others	65587_at	WW45 protein	23	111119_at	AA764217	NM_022028	NP_071311	12 C3	B	92.82%	WW domain-containing protein 3 Homolog	1	A	1.9	A	1.1	A	Biochem. Biophys. Res. Commun. 276:990-998 (2000)
17	others	65587_at	WW45 protein	24	111162_f_at	AA014158	NM_022028	NP_071311	12 C3	B	92.82%	WW domain-containing protein 3 Homolog	1	P	0.8	A	1.1	M	Biochem. Biophys. Res. Commun. 276:990-998 (2000)
17	others	65587_at	WW45 protein	25	114337_at	AW122502	NM_022028	NP_071311	12 C3	B	92.82%	WW domain-containing protein 3 Homolog	1	P	0.9	P	1.1	P	Biochem. Biophys. Res. Commun. 276:990-998 (2000)
17	others	65587_at	WW45 protein	26	112893_at	AI842198	NM_022028	NP_071311	12 C3	B	92.82%	WW domain-containing protein 3 Homolog	1.1	P	1.2	P	0.9	P	Biochem. Biophys. Res. Commun. 276:990-998 (2000)
17	others	64368_s_at	leucine-rich repeat-containing 5	27	115318_at	AI550877	-	-	-	B	90.00%	Highly similar to hypothetical protein FLJ10470 [Homo sapiens] [M.sapiens] Putative Ortholog (highly conserved)	0.2	A	0.5	A	3.4	A	-
17	others	64368_s_at	leucine-rich repeat-containing 5	28	168371_f_at	AV254278	-	-	-	C	90.00%	Highly similar to hypothetical protein FLJ10470 [Homo sapiens] [M.sapiens] Putative Ortholog (highly conserved)	1	P	1.1	P	1.2	P	-
17	others	64368_s_at	leucine-rich repeat-containing 5	29	108282_at	AA914188	-	-	-	B	90.00%	Highly similar to hypothetical protein FLJ10470 [Homo sapiens] [M.sapiens] Putative Ortholog (highly conserved)	1	P	1.5	P	1.1	P	-
17	others	64368_s_at	leucine-rich repeat-containing 5	30	108490_at	AI862388	-	-	-	C	90.00%	Highly similar to hypothetical protein FLJ10470 [Homo sapiens] [M.sapiens] Putative Ortholog (highly conserved)	1.8	A	0.8	A	1.9	P	-
17	others	64714_at	H4 histone, family 2		none								-		-		-		
17	others	65708_at	HSPC019 protein	31	114263_at	AW121271	-	-	-	B	91.43%	RIKEN cDNA 1200002H13 gene Putative Ortholog	1	P	1.2	P	1.1	P	-

Table 58

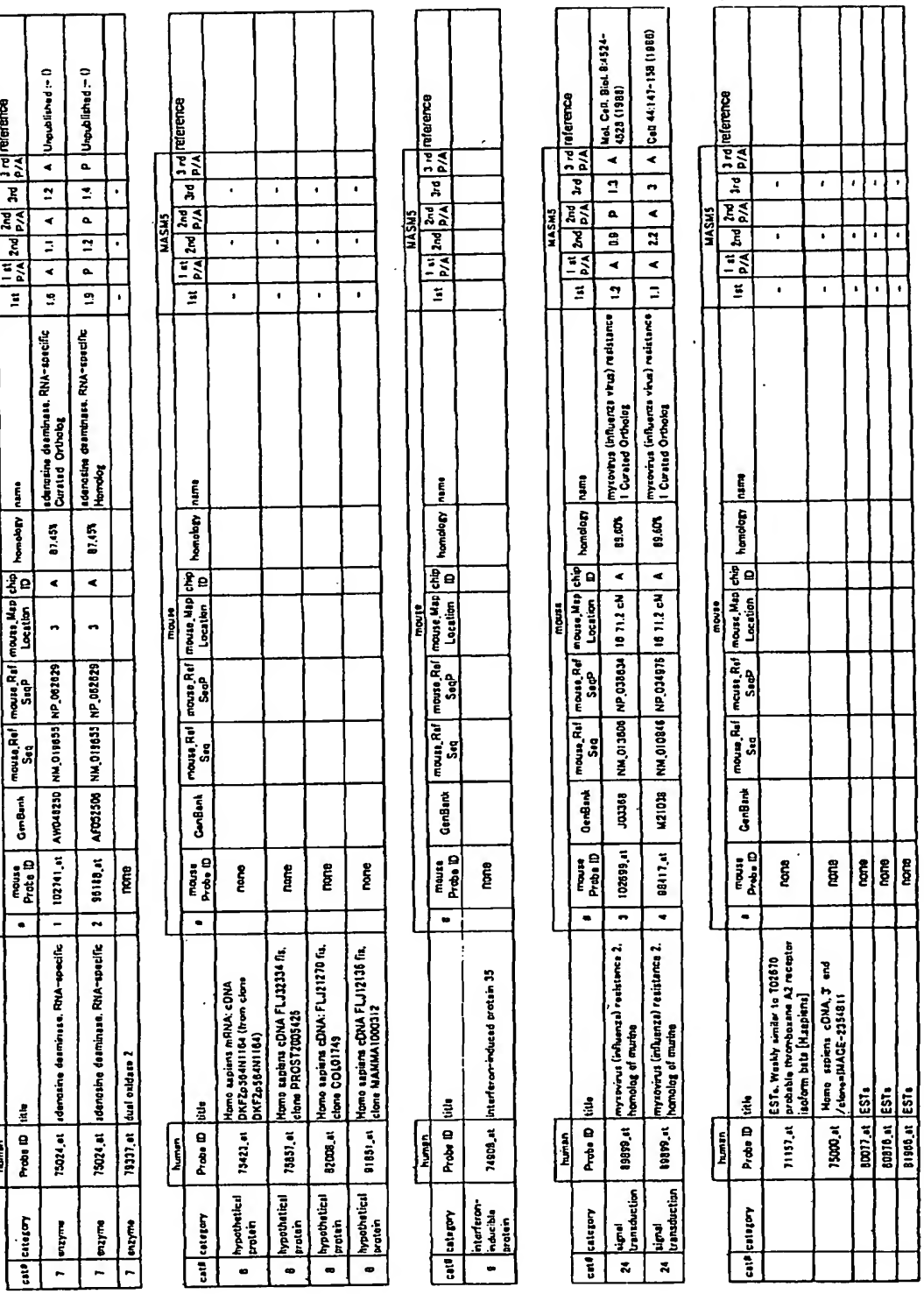
21	proteinase	63329_at	transmembrane protease, serine 2	32	109865_s_at	AA958946	NM_015775	NP_056590	16	B	85.12%	transmembrane protease, serine 2 Homolog	1.2	P	1.2	P	1.1	P	FEBS Lett. 488:93-100 (2000)
21	proteinase	63329_at	transmembrane protease, serine 2	33	131180_at	AI607826	NM_015775	NP_056590	16	C	85.12%	transmembrane protease, serine 2 Homolog	0.9	A	1.2	A	1.3	A	FEBS Lett. 488:93-100 (2000)
21	proteinase	63329_at	transmembrane protease, serine 2	34	164520_f_at	AV302474	NM_015775	NP_056590	16	B	85.12%	transmembrane protease, serine 2 Homolog	1.2	P	1.4	P	1.2	P	FEBS Lett. 488:93-100 (2000)
21	proteinase	63868_at	cathepsin C	35	101019_at	U74683	NM_009982	NP_034112	7 D3-E1.1	A		cathepsin C Curated Ortholog	1.2	P	1.1	P	1	P	Biochim. Biophys. Acta 1351 (3), 267-273 (1997)
21	proteinase	63868_at	cathepsin C	36	161251_f_at	AV316954	NM_009982	NP_034112	7 D3-E1.1	A		cathepsin C Curated Ortholog	0.7	A	1	A	1.2	A	Biochim. Biophys. Acta 1351 (3), 267-273 (1997)
21	proteinase	63868_at	cathepsin C	37	101020_at	AI842657	NM_009982	NP_034112	7 D3-E1.1	A		cathepsin C Curated Ortholog	1.8	A	0.6	A	0.9	A	Biochim. Biophys. Acta 1351 (3), 267-273 (1997)

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
24	signal transduction	63332_at	B7-H1 protein		-	AF233517	NM_021893	NP_068693	19 C2	-		programmed cell death 1 ligand 1 (Pdcd1lg1)	-		-		-		J. Exp. Med. 192 (7), 1027-1034 (2000)

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
25	structural protein	48684_at	type I intermediate filament cytokeratin	38	163187_at	AI808281	NM_033373	NP_203537	11 D	B	84.22%	type I intermediate filament cytokeratin Homolog	1.5	P	0.8	P	1.4	P	Unpublished :- ()
25	structural protein	57654_s_at	slingshot 1	39	129268_at	AW122522	-	-	-	C	92.08%	ESTs Putative Ortholog (highly conserved)	0.6	A	1	P	0.7	A	-

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
		60246_at	Homo sapiens, clone IMAGE:4428577, mRNA, partial cds	40	103066_at	L32973	NM_020557	NP_065582	12 6.0 cM	A	87.32%	thymidylate kinase family LPS-inducible member Putative Ortholog	1.3	A	2.1	A	0.7	A	Meth. Enzymol. 303:19-44 (1999)
		60246_at	Homo sapiens, clone IMAGE:4428577, mRNA, partial cds	41	161186_f_at	AV246084	NM_020557	NP_065582	12 6.0 cM	A	87.32%	thymidylate kinase family LPS-inducible member Putative Ortholog	0.8	A	1.6	A	1.4	A	Meth. Enzymol. 303:19-44 (1999)
		62330_at	ESTs		none								-		-		-		
		62828_at	ESTs		none								-		-		-		
		65457_at	ESTs		none								-		-		-		
		66392_at	ESTs		none								-		-		-		
		66899_at	ESTs		none								-		-		-		

Table 59



human				mouse							MASM5				
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3 rd P/A	reference
7	enzyme	75024_at	adenosine deaminase, RNA-specific	1	102341_at	AW048230	NM_019653	NP_062829	3	A	87.45%	adenosine deaminase, RNA-specific Curated Orthologs	1.6	A	1.1	A	1.2	A	Unpublished :- ()
7	enzyme	75024_at	adenosine deaminase, RNA-specific	2	98118_at	AF053506	NM_019653	NP_062829	3	A	87.45%	adenosine deaminase, RNA-specific Homolog	1.9	P	1.2	P	1.4	P	Unpublished :- ()
7	enzyme	79337_at	dual oxidase 2		none								-		-		-		

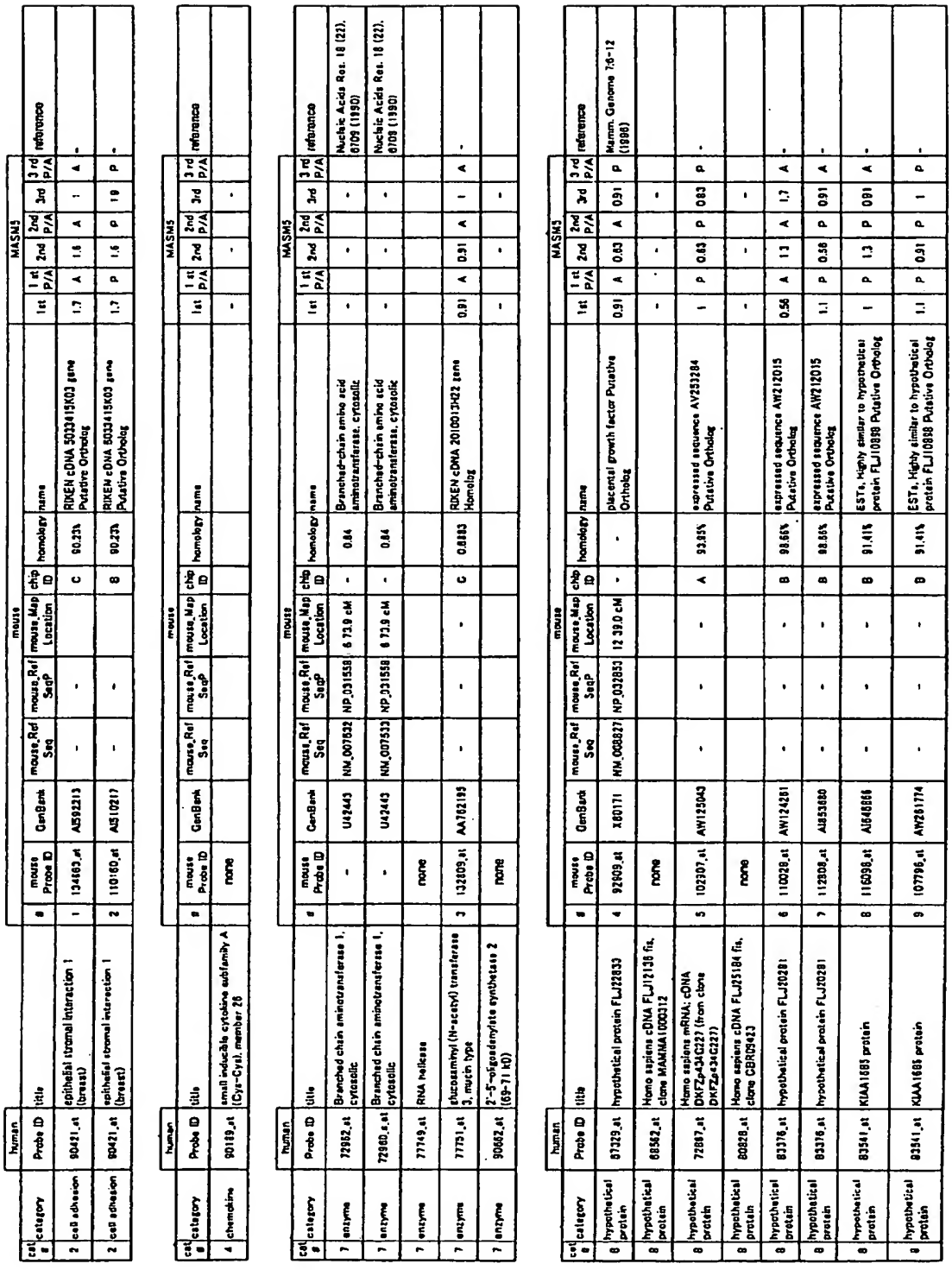
human				mouse							MASM5				
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3 rd P/A	reference
8	hypothetical protein	73421_at	Homo sapiens mRNA; cDNA DKFZp564N1164 (from clone DKFZp564N1164)		none								-		-		-		
8	hypothetical protein	78851_at	Homo sapiens cDNA FLJ32334 fis, clone PROST2005425		none								-		-		-		
8	hypothetical protein	82008_at	Homo sapiens cDNA: FLJ21270 fis, clone COL01749		none								-		-		-		
8	hypothetical protein	81851_at	Homo sapiens cDNA FLJ12136 fis, clone NAMMA1000312		none								-		-		-		

human				mouse							MASM5				
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3 rd P/A	reference
6	interferon-inducible protein	74808_at	interferon-induced protein 35		none													

human				mouse							MASM5				
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3 rd P/A	reference
24	signal transduction	89899_at	myxovirus (influenza) resistance 2, homolog of murine	3	102699_at	J00388	NM_013606	NP_038634	16 71.2 cM	A	89.60%	myxovirus (influenza virus) resistance 1 Curated Orthologs	1.2	A	0.9	P	1.3	A	Mol. Cell. Biol. 8:4524-4529 (1988)
24	signal transduction	89899_at	myxovirus (influenza) resistance 2, homolog of murine	4	88117_at	M21038	NM_010846	NP_034975	16 71.2 cM	A	89.60%	myxovirus (influenza virus) resistance 1 Curated Orthologs	1.1	A	2.2	A	3	A	Cell 44:147-158 (1986)

human				mouse							MASM5				
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3 rd P/A	reference
		71157_at	EST, Weakly similar to T03870 probable thromboxane A2 receptor isoform bta [H.sapiens]		none								-		-		-		
		75000_at	Homo sapiens cDNA, 3' end /clone=IMAGE-2354811		none								-		-		-		
		80017_at	ESTs		none								-		-		-		
		80818_at	ESTs		none								-		-		-		
		81960_at	ESTs		none								-		-		-		

Table 60



cat #	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
2	cell adhesion	90421_at	epithelial stromal interaction 1 (breast)	1	134669_at	AI592113	-	-		C	90.23%	RIKEN cDNA 5033415K03 gene Putative Ortholog	1.7	A	1.8	A	1	A	-
2	cell adhesion	90421_at	epithelial stromal interaction 1 (breast)	2	110160_at	AI510217	-	-		B	90.23%	RIKEN cDNA 5033415K03 gene Putative Ortholog	1.7	P	1.6	P	1.9	P	-

cat #	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
4	chemokine	90189_at	small inducible cytokine subfamily A (Cys-Cys), member 26		none								-		-		-		

cat #	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
7	enzyme	72952_at	Branched chain aminotransferase 1, cytosolic		-	U42443	NM_007532	NP_031558	6 73.0 cM	-	0.84	Branched-chain amino acid aminotransferase, cytosolic	-		-		-		Nucleic Acids Res. 18 (22), 6709 (1990)
7	enzyme	72960_s_at	Branched chain aminotransferase 1, cytosolic		-	U42443	NM_007533	NP_031559	6 73.0 cM	-	0.84	Branched-chain amino acid aminotransferase, cytosolic	-		-		-		Nucleic Acids Res. 18 (22), 6709 (1990)
7	enzyme	77749_at	RNA helicase		none														
7	enzyme	77751_at	glucosaminyl (N-acetyl) transferase 3, mucin type	3	132809_at	AA702193	-	-	-	C	0.8883	RIKEN cDNA 2010013H22 gene Homolog	0.91	A	0.91	A	1	A	-
7	enzyme	90682_at	2',5'-oligoadenylate synthetase 2 (69-71 kD)		none								-		-		-		

cat #	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
8	hypothetical protein	87329_at	hypothetical protein FLJ22833	4	92809_at	X60171	NM_008827	NP_032853	12 39.0 cM	-	-	placental growth factor Putative Ortholog	0.91	A	0.83	A	0.91	P	Mamm. Genome 7:6-12 (1996)
8	hypothetical protein	88562_at	Homo sapiens cDNA FLJ11138 fis, clone MAMMA1000212		none								-		-		-		
8	hypothetical protein	72887_at	Homo sapiens mRNA; cDNA DKFZp434G227 (from clone DKFZp434G227)	5	102307_at	AW125043	-	-	-	A	93.85%	expressed sequence AV253284 Putative Ortholog	1	P	0.83	P	0.83	P	-
8	hypothetical protein	80828_at	Homo sapiens cDNA FLJ25184 fis, clone CBR02623		none								-		-		-		
8	hypothetical protein	83376_at	hypothetical protein FLJ20281	6	110028_at	AW124281	-	-	-	B	98.86%	expressed sequence AW212015 Putative Ortholog	0.56	A	1.1	A	1.7	A	-
8	hypothetical protein	83376_at	hypothetical protein FLJ20281	7	112808_at	AI853880	-	-	-	B	98.86%	expressed sequence AW212015 Putative Ortholog	1.1	P	0.58	P	0.91	A	-
8	hypothetical protein	83541_at	KIAA1685 protein	8	116038_at	AI648866	-	-	-	B	91.41%	EST, Highly similar to hypothetical protein FLJ10898 Putative Ortholog	1	P	1.3	P	0.91	A	-
8	hypothetical protein	83541_at	KIAA1685 protein	9	107796_at	AW261774	-	-	-	B	91.41%	EST, Highly similar to hypothetical protein FLJ10898 Putative Ortholog	1.1	P	0.91	P	1	P	-

Table 61

8	hypothetical protein	89255_at	Homo sapiens cDNA FLJ11576 fis, clone HEMBA1003548		none								-		-		-		
8	hypothetical protein	89834_at	ESTs, Weakly similar to T22914 hypothetical protein F58E10.4 - Caenorhabditis elegans [C.elegans]	10	161376_f_at	AV243059	NM_133349	NP_579927	5	A	84.50%	expressed sequence AA407930 Putative Ortholog	1.3	A	1.7	A	0.59	A	Unpublished :- (2000)
8	hypothetical protein	89834_at	ESTs, Weakly similar to T22914 hypothetical protein F58E10.4 - Caenorhabditis elegans [C.elegans]	11	160713_at	AI841579	NM_133349	NP_579927	5	A	84.50%	expressed sequence AA407930 Putative Ortholog	0.71	A	0.83	A	1	A	Unpublished :- (2000)
8	hypothetical protein	89902_at	hypothetical protein FLJ21415	12	167609_r_at	AW121990	-	-	-	C	88.53%	RIKEN cDNA 2410131K14 gene Putative Ortholog	0.59	A	0.67	A	1	A	-
8	hypothetical protein	91420_at	hypothetical protein FLJ20989	13	94233_at	AW048642	NM_054099	NP_473440	15 D3	A	89.02%	RIKEN cDNA 1110038F14 gene Putative Ortholog	0.71	P	1.1	P	0.83	P	Meth. Enzymol. 303:19-44 (1999)

		human		mouse									MASM5						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
9	interferon-inducible protein	84893_at	viperin	14	109385_at	AI315194	NM_021384	NP_067359	12	B	85.85%	viral hemorrhagic septicemia virus(VHSV) induced gene 1 Putative Ortholog	0.77	P	1.7	P	0.28	A	J. Virol. 73:1846-1852 (1999)

		human		mouse									MASM5						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
12	membrane protein	77660_at	claudin 1	15	160415_at	AI604314	NM_016674	NP_057883	16	A	88.53%	claudin 1 Putative Ortholog (highly conserved)	1.1	A	1.6	P	1.4	P	J. Cell Biol. 141:1539-1550 (1998)
12	membrane protein	77660_at	claudin 1	16	97546_at	AF072127	NM_016674	NP_057883	16	A	88.53%	claudin 1 Putative Ortholog (highly conserved)	1.1	A	0.53	A	1.2	A	J. Cell Biol. 141:1539-1550 (1998)
12	membrane protein	86507_at	epiplakin 1		none								-		-		-		

		human		mouse									MASM5						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
16	oncogenesis	89819_at	B aggressive lymphoma gene	17	109021_at	AW214142	NM_030253	NP_084529	16 B3	B	85.82%	hypothetical protein, MGC: 7868 Putative Ortholog	1.4	P	1.6	P	1.1	P	Unpublished :- 0
16	oncogenesis	87816_g_at	malignant fibrous histiocytoma amplified sequence 1	18	163337_at	AA727483	-	-	-	B	92.68%	ESTs, Highly similar to MASL1 [H.sapiens] Putative Ortholog	0.77	P	1.1	P	1.1	P	-
16	oncogenesis	89651_at	malignant fibrous histiocytoma amplified sequence 1	18	163337_at	AA727483	-	-	-	B	92.68%	ESTs, Highly similar to MASL1 [H.sapiens] Putative Ortholog	0.77	P	1.1	P	1.1	P	-

		human		mouse									MASM5						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
17	others	80875_at	ribosomal protein L4	19	162006_r_at	AV334115	-	-	-	A	92.23%	inner membrane protein, mitochondrial Putative Ortholog	1.4	P	1.1	P	1	P	-
17	others	80875_at	ribosomal protein L4	20	100589_at	AW047808	-	-	-	A	92.23%	inner membrane protein, mitochondrial Putative Ortholog	1.8	A	1.1	A	0.91	A	-
17	others	80875_at	ribosomal protein L4	21	133128_at	AW107849	-	-	-	C	92.23%	inner membrane protein, mitochondrial Putative Ortholog	1.3	A	1.5	A	1.3	A	-
17	others	85090_at	ets homologous factor	22	102243_at	AF035527	NM_007914	NP_031940	2	A	92.68%	ets homologous factor Putative Ortholog (highly conserved)	1.9	A	1.6	A	1.8	A	Biochem. Biophys. Res. Commun. 245:176-181 (1998)

Table 62

17	others	85090_at	ets homologous factor	23	114753_at	AW215423	NM_007914	NP_031940	2	B	92.68%	ets homologous factor Putative Ortholog (highly conserved)	1.1	P	1.1	A	1.3	P	Biochem. Biophys. Res. Commun. 246:176-181 (1998)
17	others	85090_at	ets homologous factor	24	110963_at	AI527695	NM_007914	NP_031940	2	B	92.68%	ets homologous factor Putative Ortholog (highly conserved)	0.83	A	0.71	A	1	A	Biochem. Biophys. Res. Commun. 246:176-181 (1998)
17	others	85092_g_at	ets homologous factor	23	114753_at	AF035527	NM_007914	NP_031940	2	B	92.68%	ets homologous factor Putative Ortholog (highly conserved)	1.1	P	1.1	A	1.3	P	Biochem. Biophys. Res. Commun. 246:176-181 (1998)
17	others	85092_g_at	ets homologous factor	22	102243_at	AW215423	NM_007914	NP_031940	2	A	92.68%	ets homologous factor Putative Ortholog (highly conserved)	1.9	A	1.6	A	1.8	A	Biochem. Biophys. Res. Commun. 246:176-181 (1998)
17	others	85092_g_at	ets homologous factor	24	110963_at	AI527695	NM_007914	NP_031940	2	B	92.68%	ets homologous factor Putative Ortholog (highly conserved)	0.83	A	0.71	A	1.1	A	Biochem. Biophys. Res. Commun. 246:176-181 (1998)
17	others	89320_at	MKI67 (FHA domain) interacting nucleolar phosphoprotein	25	108958_at	AI851818	-	-	-	B	93.20%	RIKEN cDNA C130020J04 gene Putative Ortholog (highly conserved)	0.83	P	1.1	P	1	A	-
17	others	89320_at	MKI67 (FHA domain) interacting nucleolar phosphoprotein	26	93342_at	AI852665	-	-	-	A	93.20%	RIKEN cDNA C130020J04 gene Putative Ortholog (highly conserved)	1.3	P	0.83	P	1.1	P	-
17	others	77546_at	odd Oz/ten-m homolog 2 (Drosophila, mouse)	27	92389_at	AB025411	NM_011856	NP_035986	11 18.0 cM	A	89.61%	odd Oz/ten-m homolog 2 (Drosophila) Curated Ortholog	1.5	A	0.56	A	0.46	A	Unpublished (2001)
17	others	77546_at	odd Oz/ten-m homolog 2 (Drosophila, mouse)	28	133154_at	AW125558	-	-	-	C	95.72%	ESTs Homolog	0.67	A	0.48	A	1.4	A	-

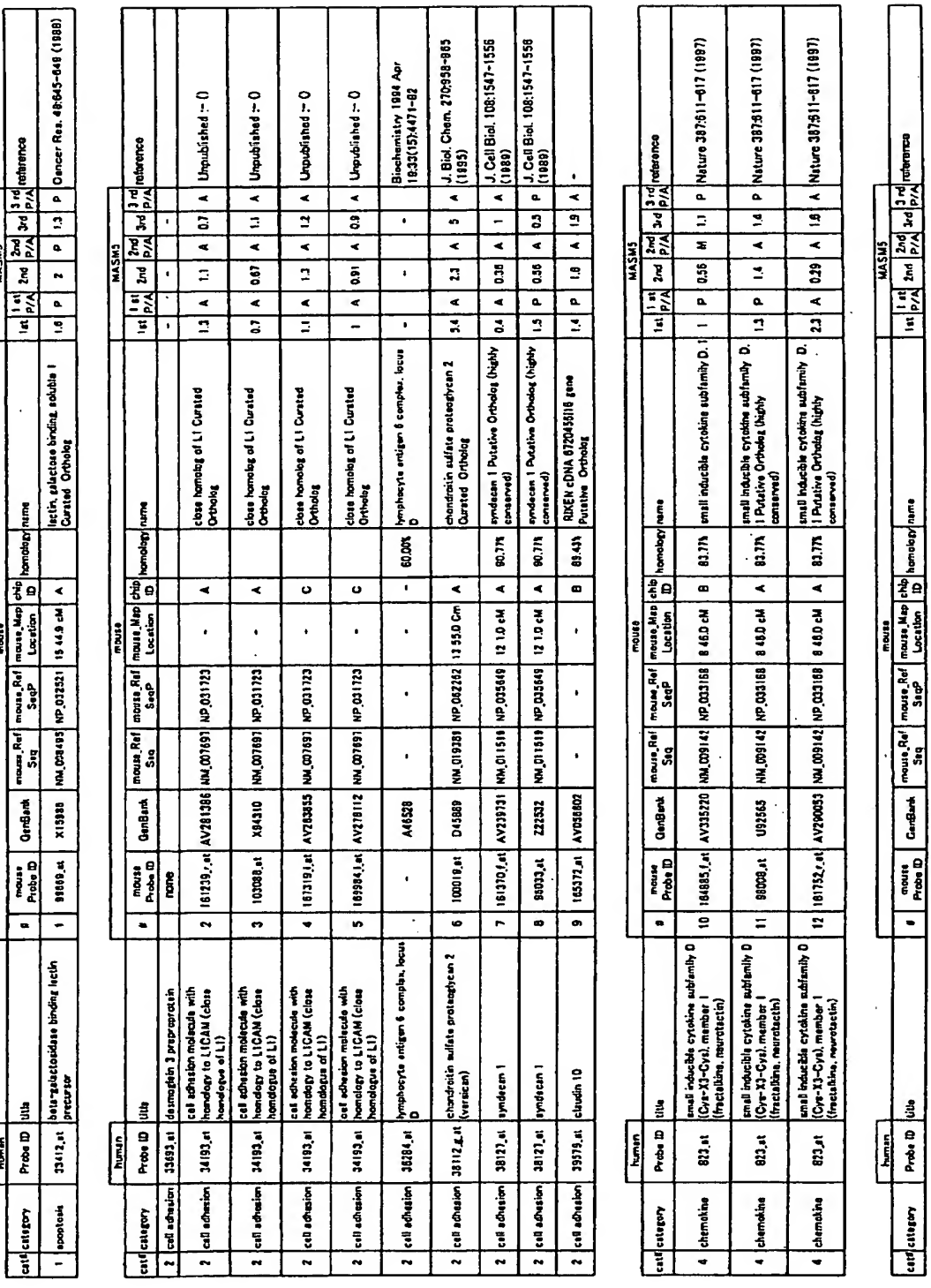
		human		mouse									MASM5						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
20	protein binding protein	89338_at	Rab coupling protein	29	135407_at	AW226597	-	-	-	C	93.75%	RIKEN cDNA 4833414G05 gene Putative Ortholog	0.77	A	2.5	A	2.1	A	-

		human		mouse									MASM5						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
24	signal transduction	87125_at	nuclear receptor co-repressor/HDAC3 complex subunit		-	AF368195	NM_030732	NP_109657	-	-		IRA1 protein (IRA1)	-		-		-		Unpublished

		human		mouse									MASM5						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
27	transporter	87860_s_at	solute carrier family 21 (organic anion transporter), member 12		none								-		-		-		
27	transporter	88617_at	solute carrier family 17 (anion/sugar transporter), member 5		none								-		-		-		

		human		mouse									MASM5						
cat #	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
		67357_at	ESTs		none								-		-		-		

Table 63



		human			mouse							MASM3							
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
1	apoptosis	33412_at	beta-galactosidase binding lectin precursor	1	98609_at	X13988	NM_008495	NP_032521	15 44.0 cM	A		lectin, galactose binding, soluble 1 (Carsted Ortholog	1.6	P	2	P	1.3	P	Cancer Res. 48:6845-849 (1988)

		human			mouse							MASM3							
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
2	cell adhesion	33693_at	desmoglein 3 preproprotein		none								-	-	-	-	-	-	
2	cell adhesion	34193_at	cell adhesion molecule with homology to L1CAM (close homologue of L1)	2	181239_r_at	AV281386	NM_007697	NP_031723	-	A		close homolog of L1 Carsted Ortholog	1.3	A	1.1	A	0.7	A	Unpublished :- ()
2	cell adhesion	34193_at	cell adhesion molecule with homology to L1CAM (close homologue of L1)	3	103088_at	X84310	NM_007697	NP_031723	-	A		close homolog of L1 Carsted Ortholog	0.7	A	0.67	A	1.1	A	Unpublished :- ()
2	cell adhesion	34193_at	cell adhesion molecule with homology to L1CAM (close homologue of L1)	4	181319_f_at	AV283955	NM_007697	NP_031723	-	C		close homolog of L1 Carsted Ortholog	1.1	A	1.3	A	1.2	A	Unpublished :- ()
2	cell adhesion	34193_at	cell adhesion molecule with homology to L1CAM (close homologue of L1)	5	189984_f_at	AV278112	NM_007697	NP_031723	-	C		close homolog of L1 Carsted Ortholog	1	A	0.91	A	0.9	A	Unpublished :- ()
2	cell adhesion	36284_at	lymphocyte antigen 6 complex, locus D		-	A46528	-	-	-	-	60.00%	lymphocyte antigen 6 complex, locus D	-		-		-		Biochemistry 1994 Apr 19;33(15):4471-82
2	cell adhesion	38112_g_at	chondroitin sulfate proteoglycan 2 (versican)	6	100019_at	D45889	NM_019389	NP_062262	13 55.0 Cm	A		chondroitin sulfate proteoglycan 2 Carsted Ortholog	3.4	A	2.3	A	5	A	J. Biol. Chem. 270:958-965 (1995)
2	cell adhesion	38121_at	syndecan 1	7	161370_f_at	AV239731	NM_011518	NP_035648	12 1.0 cM	A	80.77%	syndecan 1 Putative Ortholog (highly conserved)	0.4	A	0.38	A	1	A	J. Cell Biol. 108:1547-1556 (1989)
2	cell adhesion	38121_at	syndecan 1	8	98033_at	Z22532	NM_011518	NP_035648	12 1.0 cM	A	80.77%	syndecan 1 Putative Ortholog (highly conserved)	1.5	P	0.56	A	0.5	P	J. Cell Biol. 108:1547-1556 (1989)
2	cell adhesion	39379_at	claudin 10	9	165372_at	AV036802	-	-	-	B	89.43%	RIKEN cDNA 6720455I16 gene Putative Ortholog	1.4	P	1.8	A	1.9	A	-

		human			mouse							MASM3							
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
4	chemokine	823_at	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)	10	184885_f_at	AV335220	NM_009142	NP_033168	8 46.0 cM	B	83.77%	small inducible cytokine subfamily D. 1	1	P	0.56	M	1.1	P	Nature 387:611-617 (1997)
4	chemokine	823_at	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)	11	98008_at	U92565	NM_009142	NP_033168	8 46.0 cM	A	83.77%	small inducible cytokine subfamily D. 1 Putative Ortholog (highly conserved)	1.3	P	1.4	A	1.4	P	Nature 387:611-617 (1997)
4	chemokine	823_at	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)	12	181752_r_at	AV290053	NM_009142	NP_033168	8 46.0 cM	A	83.77%	small inducible cytokine subfamily D. 1 Putative Ortholog (highly conserved)	2.3	A	0.29	A	1.8	A	Nature 387:611-617 (1997)

		human			mouse							MASM3							
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference

Table 64

5	cytokine related	1385_at	transforming growth factor, beta-induced, 68kD	13	161167_r_at	AV231282	NM_009369	NP_033395	13 38.0 cM	A	88.65%	transforming growth factor, beta induced, 68 kDa Homolog	1.6	A	1.9	A	0.4	A	DNA Cell Biol. 13:571-584(1994)
5	cytokine related	1385_at	transforming growth factor, beta-induced, 68kD	14	92877_at	L19932	NM_009369	NP_033395	13 38.0 cM	A	88.65%	transforming growth factor, beta induced, 68 kDa Homolog	1.3	P	1.8	P	0.9	P	DNA Cell Biol. 13:571-584(1994)
5	cytokine related	38631_at	tumor necrosis factor, alpha-induced protein 2	15	160489_at	L24118	NM_009369	NP_033395	13 38.0 cM	A	83.11%	tumor necrosis factor, alpha-induced protein 2 Putative Ortholog	0.6	A	0.67	A	0.6	A	DNA Cell Biol. 13:571-584(1994)

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
6	cytosolic protein	35275_at	adaptor-related protein complex 1, gamma 1 subunit	16	161593_r_at	AV291690	-	-	-	A	93.61%	adaptor protein complex AP-1, gamma 1 subunit Putative Ortholog (highly conserved)	0.6	A	0.22	A	0.7	A	-
6	cytosolic protein	35275_at	adaptor-related protein complex 1, gamma 1 subunit	17	103242_at	AW123834	NM_009677	NP_033807	-	A	93.61%	adaptor protein complex AP-1, gamma 1 subunit Putative Ortholog (highly conserved)	1.1	P	1.2	P	0.8	P	J. Cell Biol. 111:2319-2326 (1990)
6	cytosolic protein	35275_at	adaptor-related protein complex 1, gamma 1 subunit	18	92288_at	X54424	NM_009677	NP_033807	-	A	93.61%	adaptor protein complex AP-1, gamma 1 subunit Putative Ortholog (highly conserved)	1	P	0.63	A	1.2	P	J. Cell Biol. 111:2319-2326 (1990)
6	cytosolic protein	40508_at	glutathione S-transferase A4		none								-		-		-		

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
7	enzyme	32805_at	hepatic dihydrodiol dehydrogenase gene, exon 9		none								-		-		-		
7	enzyme	34637_f_at	class I alcohol dehydrogenase, alpha subunit	19	94906_at	M22679	NM_007409	NP_031435	3 71.2 cM	A		alcohol dehydrogenase 1, complex Curated Ortholog	0.6	P	0.29	P	0.5	P	Proc. Natl. Acad. Sci. U.S.A. 82:2262-2266 (1985)
7	enzyme	34935_at	dJ127D3.3 (Flavin-containing Monooxygenase 2)	20	106011_at	AW261476	NM_018881	NP_061369	-	B	86.79%	flavin containing monooxygenase 2 Curated Ortholog	0.7	P	0.53	P	0.9	P	Genome Res. 10:1617-1630 (2000)
7	enzyme	35947_at	keratinocyte transglutaminase gene	21	165790_at	AA681923	NM_019984	NP_064368	-	C		transglutaminase 1, K polypeptide Curated Ortholog	1.2	A	0.46	A	1	A	J. Biol. Chem. 274:34148-34154 (1999)
7	enzyme	36247_f_at	class I alcohol dehydrogenase, gamma subunit	19	94906_at	M22679	NM_007409	NP_031435	3 71.2 cM	A	84.57%	alcohol dehydrogenase 1, complex Putative Ortholog	0.6	P	0.29	P	0.5	P	Proc. Natl. Acad. Sci. U.S.A. 82:2262-2266 (1985)
7	enzyme	36454_at	carbonic anhydrase XII precursor	22	103905_at	AI314958	-	-	-	A	94.05%	RIKEN cDNA 2310047E01 gene Putative Ortholog	0.6	A	0.59	A	1	A	-
7	enzyme	36658_at	selectin-1		none								-		-		-		
7	enzyme	37215_at	glycogen phosphorylase	23	164478_r_at	AV246818	NM_133198	NP_573461	12 30.0 cM	B		liver glycogen phosphorylase Curated Ortholog	1.1	A	1.6	A	1.3	A	Unpublished :- (2001)
7	enzyme	37215_at	glycogen phosphorylase	24	110291_at	AI256160	NM_133198	NP_573461	12 30.0 cM	B		liver glycogen phosphorylase Curated Ortholog	0.9	P	1.3	P	1.2	P	Unpublished :- (2001)
7	enzyme	37415_at	ATPase, Class V, type 10B		none								-		-		-		
7	enzyme	37700_at	bleomycin hydrolase	25	162221_i_at	AV112892	-	-	-	A	91.80%	clone MGC:37104 IMAGE:4952098, mRNA, complete cds Putative Ortholog	1.1	M	1.3	A	1	A	-
7	enzyme	37700_at	bleomycin hydrolase	26	94842_at	AI853830	-	-	-	A	91.80%	clone MGC:37104 IMAGE:4952098, mRNA, complete cds Putative Ortholog	0.8	P	0.909	P	1.2	P	-

Table 65

7	enzyme	37700_at	bleomycin hydrolase	27	162179_r_at	AV367224	-	-	-	A	91.80%	clone MGC:37104 IMAGE:4952098, mRNA, complete cds Putative Ortholog	1.1	A	1.2	A	1.4	A	-
7	enzyme	37956_at	aldehyde dehydrogenase 3B2		none								-		-		-		
7	enzyme	38285_at	crystallin, mu	28	160937_at	AF039391	NM_016669	NP_057878	7 55.0 cM	A		crystallin, mu Curated Ortholog	1.9	A	0.91	A	0.6	A	Unpublished :- ()
7	enzyme	38285_at	crystallin, mu	29	166000_at	AV248813	NM_016669	NP_057878	7 55.0 cM	C		crystallin, mu Curated Ortholog	1.3	A	0.59	A	0.4	A	Unpublished :- ()
7	enzyme	38790_at	epoxide hydrolase 1, microsomal (xenobiotic)	30	101587_at	U89419	NM_010145	NP_034275	1 98.5 cM	A		epoxide hydrolase 1, microsomal Curated Ortholog	0.5	P	0.04	A	0.4	P	Genome Res. 10:1617-1630 (2000)
7	enzyme	39008_at	ceruloplasmin (ferroxidase)	31	92851_at	U49430	NM_007752	NP_031778	9 55.0 cM	A		ceruloplasmin Curated Ortholog	1.8	P	3.1	P	2.2	P	J. Clin. Invest. 98:207-215 (1996)
7	enzyme	39317_at	cytidine monophospho-N-acetylneuraminic acid hydroxylase	32	93588_at	D21826	NM_007717	NP_031743	-	A		cytidine monophospho-N-acetylneuraminic acid hydroxylase Curated Ortholog	0.2	A	2.5	A	1.9	A	J. Biol. Chem. 270:16458-16463 (1995)
7	enzyme	40082_at	long-chain fatty-acid-Coenzyme A ligase 2	33	94507_at	U15977	NM_007981	NP_032007	-	A		fatty acid Coenzyme A ligase, long chain 2 Curated Ortholog	0.6	P	0.83	P	1	P	Genome Res. 10:1617-1630 (2000)
7	enzyme	40522_at	glutamate-ammonia ligase (glutamine synthase)	34	117284_at	AI848384	NM_008131	NP_032157	-	B	89.74%	glutamine synthetase Curated Ortholog	0.8	P	0.63	P	1.9	P	J. Mol. Biol. 208:45-58 (1989)
7	enzyme	40522_at	glutamate-ammonia ligase (glutamine synthase)	35	99498_at	M60803	NM_008131	NP_032157	-	A	89.74%	glutamine synthetase pseudogene 1 Homolog	0.4	A	0.77	A	1.3	A	J. Mol. Biol. 208:45-56 (1989)
7	enzyme	40522_at	glutamate-ammonia ligase (glutamine synthase)	36	94852_at	U09114	NM_008131	NP_032157	-	A	89.74%	glutamine synthetase Homolog	0.9	P	0.77	P	1	P	J. Mol. Biol. 208:45-58 (1989)
7	enzyme	40522_at	glutamate-ammonia ligase (glutamine synthase)	37	161826_r_at	AV381947	NM_008131	NP_032157	-	A	89.74%	glutamine synthetase Homolog	1.2	P	0.91	P	1.2	P	J. Mol. Biol. 208:45-56 (1989)
7	enzyme	40665_at	flavin containing monooxygenase 3	38	101991_at	D16215	NM_010231	NP_034361	-	A	85.71%	flavin containing monooxygenase 1 Homolog	1.1	P	0.71	P	0.8	P	Unpublished :- ()
7	enzyme	40665_at	flavin containing monooxygenase 3	39	104421_at	U87147	NM_008030	NP_032056	-	A		flavin containing monooxygenase 3 Curated Ortholog	0.4	P	0.27	P	0.4	P	Arch. Biochem. Biophys. 347:9-18 (1997)
7	enzyme	770_at	plasma glutathione peroxidase 3 precursor	40	168706_r_at	AV225591	NM_008161	NP_032187	-	C		glutathione peroxidase 3 Curated Ortholog	0.2	A	1.1	A	3.2	A	J. Biol. Chem. 269:27066-27073 (1994)
7	enzyme	770_at	plasma glutathione peroxidase 3 precursor	41	101676_at	U13705	NM_008161	NP_032187	-	A		glutathione peroxidase 3 Curated Ortholog	0.9	P	0.91	P	0.8	P	J. Biol. Chem. 269:27066-27073 (1994)

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
8	hypothetical protein	32215_i_at	KIAA0878 protein	42	113969_at	AW208826	-	-	-	B	94.02%	RIKEN cDNA 2610033K01 gene Putative Ortholog	0.7	P	0.83	A	0.8	P	-
8	hypothetical protein	39400_at	KIAA1055 protein		none								-		-		-		
8	hypothetical protein	39597_at	KIAA0843 protein	43	135495_r_at	AV242700	-	-	-	C	98.00%	ESTs, Weakly similar to A28490 DNA-directed RNA polymerase [M.musculus] Putative Ortholog	0.9	A	0.83	A	1.3	P	-
8	hypothetical protein	39597_at	KIAA0843 protein	44	162910_at	AI227478	-	-	-	B	96.00%	ESTs, Weakly similar to A28490 DNA-directed RNA polymerase [M.musculus] Putative Ortholog	0.9	P	0.87	P	0.4	A	-
8	hypothetical protein	39597_at	KIAA0843 protein	45	112372_at	AW230421	-	-	-	B	98.00%	ESTs, Weakly similar to A28490 DNA-directed RNA polymerase [M.musculus] Putative Ortholog	0.7	P	0.50	P	0.8	P	-

Table 66

8	hypothetical protein	40943_at	long-chain fatty-acyl elongase	46	108490_at	AI463227	-	-	-	B	99.19%	long chain fatty acyl elongase Putative Ortholog	1	P	1.1	P	1	P	-
8	hypothetical protein	40943_at	long-chain fatty-acyl elongase	47	94418_at	AI839004	NM_130450	NP_569717	-	A	99.19%	long chain fatty acyl elongase Putative Ortholog	0.4	A	1.7	P	1.7	P	Unpublished :- (2001)

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
10	kinase	1108_s_at	EphA1	48	169261_at	AV298003	NM_023580	NP_076069	-	C	92.55%	Eph receptor A1 Curated Ortholog	0.9	M	0.91	A	0.7	A	Proc. Natl. Acad. Sci. U.S.A.93:145-150 (1996)
10	kinase	1108_s_at	EphA1	49	100143_at	Y07711	NM_011777	NP_035907	-	A	92.55%	zyxin Putative Ortholog	3.3	A	1.5	A	0.8	A	J. Biol. Chem. 271:31470-31478 (1996)
10	kinase	33804_at	protein tyrosine kinase 2 beta	50	103451_at	AI835159	-	-	-	A		protein tyrosine kinase 2 beta Curated Ortholog	1.3	P	1.2	P	1.1	P	-
10	kinase	33804_at	protein tyrosine kinase 2 beta	51	169902_at	AV214820	-	-	-	C	93.42%	RIKEN cDNA 2310057D15 gene Putative Ortholog	1.3	A	1.6	A	1.6	A	-
10	kinase	33804_at	protein tyrosine kinase 2 beta	52	167168_f_at	AV127592	-	-	-	C	93.42%	RIKEN cDNA 2310057D15 gene Putative Ortholog	1	P	1.2	P	0.9	P	-
10	kinase	33804_at	protein tyrosine kinase 2 beta	53	160057_at	AW125329	-	-	-	A	93.42%	RIKEN cDNA 2310057D15 gene Putative Ortholog	1	A	1.6	A	1	A	-
10	kinase	36502_at	PFTAIRE protein kinase 1	54	93422_at	U62391	NM_011074	NP_035204	5 0.0 cM	A	94.21%	PFTAIRE protein kinase 1 Putative Ortholog (highly conserved)	1.5	P	0.71	A	1.3	P	J. Neurochem. 69:348-364 (1997)
10	kinase	36502_at	PFTAIRE protein kinase 1	55	93421_at	AF033655	NM_011074	NP_035204	5 0.0 cM	A	94.21%	PFTAIRE protein kinase 1 Putative Ortholog (highly conserved)	0.8	P	0.71	P	0.6	P	J. Neurochem. 69:348-364 (1997)
10	kinase	36502_at	PFTAIRE protein kinase 1	56	158913_r_at	AV347594	NM_011074	NP_035204	5 0.0 cM	C	94.21%	PFTAIRE protein kinase 1 Putative Ortholog	0.8	A	0.77	A	0.7	A	J. Neurochem. 69:348-364 (1997)
10	kinase	36502_at	PFTAIRE protein kinase 1	57	157725_f_at	AI847882	NM_011074	NP_035204	5 0.0 cM	C	94.21%	PFTAIRE protein kinase 1 Putative Ortholog	0.8	P	0.83	P	0.7	P	J. Neurochem. 69:348-364 (1997)
10	kinase	39120_at	metallothionein 1L	58	113152_at	AI850672	NM_016866	NP_058562	-	B	93.22%	serine/threonine kinase 39, STE20/SPS1 homolog (yeast) Putative Ortholog (highly conserved)	1	P	0.32	A	1	A	Oncogene 19:4290-4297 (2000)
10	kinase	39120_at	metallothionein 1L	59	160808_at	AF099988	NM_016866	NP_058562	-	A	93.22%	serine/threonine kinase 39, STE20/SPS1 homolog (yeast) Putative Ortholog (highly conserved)	1.6	P	0.56	A	0.9	P	Oncogene 19:4290-4297 (2000)

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
11	matrix protein	36881_at	electron-transfer-flavoprotein, beta polypeptide	60	95947_at	AW046273	-	-	-	A	87.45%	RIKEN cDNA 0610009I16 gene Putative Ortholog (highly conserved)	0.9	P	1.1	P	1.1	P	-
11	matrix protein	36881_at	electron-transfer-flavoprotein, beta polypeptide	61	162144_at	AV351508	-	-	-	A	87.45%	RIKEN cDNA 0610009I16 gene Putative Ortholog (highly conserved)	1.6	P	1	P	0.8	M	-
11	matrix protein	36881_at	electron-transfer-flavoprotein, beta polypeptide	62	107600_at	AI838753	-	-	-	B		RIKEN cDNA 4921504I16 gene Curated Ortholog	0.8	P	0.77	P	0.9	P	-
11	matrix protein	37600_at	extracellular matrix protein 1, isoform 1, 2	63	98054_at	L33416	NM_007899	NP_031925	3 45.4 cM	A	86.72%	extracellular matrix protein 1 Homolog	0.9	A	1.3	A	1.5	A	Gene 226:253-261 (1999)
11	matrix protein	37600_at	extracellular matrix protein 1, isoform 1, 2	64	170917_r_at	AV092620	NM_007899	NP_031925	3 45.4 cM	C	86.72%	extracellular matrix protein 1 Homolog	0.3	A	1.4	A	2.3	A	Gene 226:253-261 (1999)
11	matrix protein	37600_at	extracellular matrix protein 1, isoform 1, 2	65	160641_at	AI021573	NM_133232	NP_573495	-	A	93.10%	inducible 6-phosphofructo-2-kinase Putative Ortholog	0.9	A	0.83	P	0.6	A	Unpublished :- ()

Table 67

11	matrix protein	37600_at	extracellular matrix protein 1, isoform 1, 2	66	103577_at	AI326331	NM_133232	NP_573415	-	A	93.10%	Inducible 6-phosphofructo-2-kinase Putative Ortholog	0.6	A	0.5	A	1.3	A	Unpublished :- 0

		human		mouse									MASMS						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
12	membrane protein	1042_at	retinoic acid receptor responder (tazarotene induced) 1	67	116451_at	AA615200	-	-	-	B	87.74%	expressed sequence AI882122 Putative Ortholog (highly conserved)	0.8	A	0.5	A	0.8	A	-
12	membrane protein	33505_at	retinoic acid receptor responder (tazarotene induced) 1	67	116451_at	AA615200	-	-	-	B	87.74%	expressed sequence AI882122 Putative Ortholog (highly conserved)	0.8	A	0.5	A	0.8	A	-
12	membrane protein	33331_at	BENE protein		none								-		-		-		
12	membrane protein	33782_at	prostate stem cell antigen	68	160508_at	AW209488	-	-	-	A	80.69%	prostate stem cell antigen Putative Ortholog	1	A	0.71	A	1.3	A	-
12	membrane protein	34280_at	Homo sapiens mRNA for putative GABA receptor epsilon subunit		-	AH009304	NM_017369	NP_059065	-	-	84.80%	gamma-aminobutyric acid (GABA-A) receptor, subunit	-		-		-		Neurosci 2000 May 15;20(10):3588-95
12	membrane protein	34288_at	G protein-coupled receptor	69	93430_at	AF000236	NM_007722	NP_031748	1 55.6 cM	A	89.09%	chemokine orphan receptor 1 Putative Ortholog (highly conserved)	0.7	M	0.29	P	0.6	P	Immunogenetics :- (1997)
12	membrane protein	34898_at	amphiregulin (schwannoma-derived growth factor)	70	99915_at	L41352	NM_009704	NP_033834	5 51.0 cM	A	83.58%	amphiregulin Homolog	0.8	M	0.56	A	0.7	A	Biochem. Biophys. Res. Commun. 185:103-109 (1992)
12	membrane protein	38223_at	vascular Rab-GAP/TBC-containing	71	96339_at	AW048383	NM_053257	NP_444487	-	A	95.63%	ribosomal protein L31 Putative Ortholog	0.5	A	0.91	A	0.6	A	Meth. Enzymol. 303:19-44 (1999)
12	membrane protein	38223_at	vascular Rab-GAP/TBC-containing	72	157252_at	AV108158	NM_053257	NP_444487	-	C	95.63%	ribosomal protein L31 Putative Ortholog	0.5	A	1.6	A	1.3	A	Meth. Enzymol. 303:19-44 (1999)
12	membrane protein	38223_at	vascular Rab-GAP/TBC-containing	73	164621_i_at	AV157335	NM_053257	NP_444487	-	B	95.63%	ribosomal protein L31 Putative Ortholog	0.9	P	1.1	P	1	P	Meth. Enzymol. 303:19-44 (1999)
12	membrane protein	38379_at	glycoprotein (transmembrane) nmb	74	108822_at	AI615758	NM_053110	NP_444340	6 21.0 cM	B	81.15%	glycoprotein (transmembrane) nmb Putative Ortholog (highly conserved)	1.1	M	1.1	M	1.7	A	J. Biol. Chem. 276:8125-8134 (2001)
12	membrane protein	38379_at	glycoprotein (transmembrane) nmb	75	168824_at	AV223501	NM_053110	NP_444340	6 21.0 cM	C	81.15%	glycoprotein (transmembrane) nmb Putative Ortholog (highly conserved)	2.8	A	0.63	A	0.7	A	J. Biol. Chem. 276:8125-8134 (2001)
12	membrane protein	38750_at	Notch homolog 3	76	92956_at	X74760	NM_008716	NP_032742	17 20.0 cM	A	84.91%	Notch gene homolog 3, (Drosophila) Putative Ortholog	0.7	P	0.5	P	0.8	P	Mech. Dev. 46:123-138 (1994)
12	membrane protein	39310_at	bradykinin receptor B2	77	98387_at	L26047	NM_009747	NP_033877	12 53.0 cM	A	85.67%	bradykinin receptor, beta 2 Putative Ortholog (highly conserved)	0.6	A	0.42	A	0.6	A	Mol. Pharmacol. 44:346-355 (1993)
12	membrane protein	40990_at	tetraspan 5	78	129282_at	AW124518	NM_019571	NP_062517	-	C	93.28%	transmembrane 4 superfamily member 9 Putative Ortholog	0.8	A	1	P	0.8	A	Genome Res. 10:1617-1630 (2000)
12	membrane protein	40990_at	tetraspan 5	79	140325_at	AW125637	NM_019571	NP_062517	-	C	93.28%	transmembrane 4 superfamily member 9 Putative Ortholog	1.5	A	1.2	A	1.2	A	Genome Res. 10:1617-1630 (2000)
12	membrane protein	40990_at	tetraspan 5	80	163391_at	AW123971	NM_019571	NP_062517	-	B	93.28%	transmembrane 4 superfamily member 9 Putative Ortholog	1	P	0.83	P	0.9	P	Genome Res. 10:1617-1630 (2000)
12	membrane protein	40990_at	tetraspan 5	81	92426_at	AI877157	NM_019571	NP_062517	-	A	93.28%	transmembrane 4 superfamily member 9 Putative Ortholog	0.6	A	2.7	A	0.4	A	Genome Res. 10:1617-1630 (2000)

		human		mouse									MASMS						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
13	metabolism	32249_at	annexin A10	85	92494_at	AJ238978	NM_011922	NP_036052	8 32.0 cM	A	87.74%	annexin A10 Putative Ortholog	1.8	A	1.3	A	0.9	A	Meth. Enzymol. 303:19-44 (1999)

Table 68

13	metabolism	32464_at	defensin, beta 2		-	AJ011800	NM_010030	NP_034160	8 9.0 cM	-		defensin beta 2 (Defb2)	-		-		-		FEBS Lett 1999 Jan 8;442(1):112-6
13	metabolism	35496_at	inositol(myo)-1(or 4)-monophosphatase 2	83	98420_at	AA919924	NM_053261	NP_44449	-	A	88.21%	Mus musculus myo-inositol monophosphatase 2 (Impa2) mRNA, complete cds Putative Ortholog (highly conserved)	0.5	A	1.7	A	0.8	A	Gene 271:285-291 (2001)
13	metabolism	37399_at	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)		AI605678	-	-	-	-	-	86.00%	ESTs, Weakly similar to DHBX_MOUSE Estradiol 17							-
13	metabolism	37482_at	aldo-keto reductase family 1, member B10 (aldose reductase)	84	161918_at	AV380611	NM_009731	NP_033861	6 14.0 cM	A		androgen regulated vas deferens protein Curated Ortholog	0.7	A	0.59	A	1.7	A	J. Biol. Chem. 265:19932-19936 (1993)
13	metabolism	37482_at	aldo-keto reductase family 1, member B10 (aldose reductase)	85	102826_at	J05663	NM_009731	NP_033861	6 14.0 cM	A		androgen regulated vas deferens protein Curated Ortholog	1.4	A	0.42	A	0.9	A	J. Biol. Chem. 265:19932-19936 (1993)
13	metabolism	37482_at	aldo-keto reductase family 1, member B10 (aldose reductase)	86	132885_at	AI429094	-	-	-	C	89.66%	ESTs, Moderately similar to ALDOSE REDUCTASE-RELATED PROTEIN 2 [M.musculus] Homolog	0.7	A	1.6	A	0.4	A	-
13	metabolism	39789_at	fatty acid binding protein 5 (psoriasis-associated)	87	160544_at	AJ223066	NM_010634	NP_034764	-	A	82.76%	fatty acid binding protein 5, epidermal Putative Ortholog	1.3	P	0.56	P	1.2	P	J. Biol. Chem. 268:17362-17369 (1999)
13	metabolism	39789_at	fatty acid binding protein 5 (psoriasis-associated)	88	109764_at	AI840194	NM_010634	NP_034764	-	B	82.76%	fatty acid binding protein 5, epidermal Putative Ortholog	0.2	A	2.7	P	0.8	A	J. Biol. Chem. 268:17362-17369 (1999)

		human		mouse									MASMS						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
14	MHC	38095_i_at	major histocompatibility complex, class II, DP beta 1	89	100998_at	M21932	NM_010379	NP_034509	17 18.84 cM	A	91.18%	histocompatibility 2, class II antigen A, beta 1 Putative Ortholog	1.1	P	1.6	P	1.7	P	Cell 34:179-188 (1983)
14	MHC	38095_i_at	major histocompatibility complex, class II, DP beta 1	90	116266_at	AW122580	NM_010382	NP_034512	17 18.86 cM	B	91.23%	histocompatibility 2, class II antigen A, beta 1 Putative Ortholog	0.7	A	1.5	A	1.7	A	Proc. Natl. Acad. Sci. U.S.A. 80:7621-7625 (1983)
14	MHC	38096_f_at	major histocompatibility complex, class II, DP beta 1	89	100998_at	M21932	NM_010379	NP_034509	17 18.84 cM	A	91.18%	histocompatibility 2, class II antigen A, beta 1 Putative Ortholog	1.1	P	1.8	P	1.7	P	Cell 34:179-188 (1983)
14	MHC	38096_f_at		90	116266_at	AW122580	NM_010382	NP_034512	17 18.86 cM	B	91.23%	histocompatibility 2, class II antigen A, beta 1 Putative Ortholog	0.7	A	1.5	A	1.7	A	Proc. Natl. Acad. Sci. U.S.A. 80:7621-7625 (1983)

		human		mouse									MASMS						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
15	MMP related	1006_at	matrix metalloproteinase 10 preproprotein	91	94724_at	Y13185	NM_019471	NP_062344	-	A	84.75%	matrix metalloproteinase 10 Putative Ortholog (highly conserved)	1.4	A	1.2	A	1.2	A	J. Biol. Chem. 269 (14), 10383-10389 (1994)
15	MMP related	31859_at	matrix metalloproteinase 9 preproprotein	92	162369_f_at	AV239570	NM_013599	NP_038627	2 86.0 cM	A	83.10%	matrix metalloproteinase 9 Putative Ortholog (highly conserved)	2	A	1.8	A	1.2	A	Biochem. Biophys. Res. Commun. 190:732-740 (1993)
15	MMP related	31859_at	matrix metalloproteinase 9 preproprotein	93	99957_at	X72795	NM_013599	NP_038627	2 86.0 cM	A	83.10%	matrix metalloproteinase 9 Putative Ortholog (highly conserved)	1	A	1.5	A	0.4	A	Biochem. Biophys. Res. Commun. 190:732-740 (1993)
15	MMP related	31859_at	matrix metalloproteinase 9 preproprotein	94	188521_r_at	AV231880	NM_013599	NP_038627	2 86.0 cM	C	83.10%	matrix metalloproteinase 9 Curated Ortholog	1.9	A	0.53	A	1	A	Biochem. Biophys. Res. Commun. 190:732-740 (1993)

		human		mouse									MASMS						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference

Table 69

16	oncogenesis	1915_s_at	cellular oncogene c-fos (complete sequence)	95	161716_at	AV252296	NM_010234	NP_034364	12 40.0 cM	A		FBJ osteosarcoma oncogene Curated Ortholog	0.7	A	1	A	0.7	A	Cell 32:1241-1255 (1983)
16	oncogenesis	1915_s_at	cellular oncogene c-fos (complete sequence)	96	160901_at	V00727	NM_010234	NP_034364	12 40.0 cM	A	91.42%	FBJ osteosarcoma oncogene Homolog	0.7	P	0.77	P	0.7	P	Cell 32:1241-1255 (1983)
16	oncogenesis	1915_s_at	cellular oncogene c-fos (complete sequence)	97	167990_at	AA118815	-	-	-	C	91.40%	RIKEN cDNA 4933433D06 gene Putative Ortholog	1	A	0.53	A	2.3	A	-
16	oncogenesis	1916_s_at	cellular oncogene c-fos (complete sequence)	95	161716_at	AV252296	NM_010234	NP_034364	12 40.0 cM	A		FBJ osteosarcoma oncogene Curated Ortholog	0.7	A	1	A	0.7	A	Cell 32:1241-1255 (1983)
16	oncogenesis	1916_s_at	cellular oncogene c-fos (complete sequence)	96	160901_at	V00727	NM_010234	NP_034364	12 40.0 cM	A	91.42%	FBJ osteosarcoma oncogene Homolog	0.7	P	0.77	P	0.7	P	Cell 32:1241-1255 (1983)
16	oncogenesis	1916_s_at	cellular oncogene c-fos (complete sequence)	97	167890_at	AA118815	-	-	-	C	91.49%	RIKEN cDNA 4933433D06 gene Putative Ortholog	1	A	0.53	A	2.3	A	-
16	oncogenesis	36933_at	N-myc downstream regulated gene 1	98	93506_at	AW121063	NM_133668	NP_598429	-	A	91.26%	solute carrier family 25 (mitochondrial carrier adenine nucleotide translocator), member 3 Putative Ortholog	2.9	A	0.71	A	0.4	A	Unpublished :- (2001)
16	oncogenesis	36933_at	N-myc downstream regulated gene 1	99	160464_s_at	U60593	NM_101088 4	NP_035014	downstream of N-myc	A		N-myc downstream regulated 1 Curated Ortholog	0.5	A	0.56	A	1.1	A	Mech. Dev. 831-2 (1999)
16	oncogenesis	37283_at	meningioma 1	100	110774_at	AI852667	-	-	-	B	87.26%	ESTs, Weakly similar to MN1_HUMAN PROBABLE TUMOR SUPPRESSOR PROTEIN MN1[H.sapiens] Putative Ortholog	0.6	A	0.56	A	2.3	A	-
16	oncogenesis	37821_at	breast carcinoma amplified sequence 1	101	163288_at	AW122051	-	-	-	B	85.79%	RIKEN cDNA 2210416M21 gene Homolog	0.8	A	0.67	A	0.8	A	-
16	oncogenesis	38827_at	anterior gradient 2 homolog (Xenepus laevis)	102	101076_r_at	AB016592	NM_011783	NP_035913	-	A	88.15%	anterior gradient 2 (Xenopus laevis) Putative Ortholog	0.6	A	0.91	A	1	A	Biochem. Biophys. Res. Commun. 251:111-116 (1998)
16	oncogenesis	38827_at	anterior gradient 2 homolog (Xenepus laevis)	103	101075_f_at	AB016592	NM_011783	NP_035913	-	A	88.15%	anterior gradient 2 (Xenopus laevis) Putative Ortholog	8.4	P	11.8	P	21	P	Biochem. Biophys. Res. Commun. 251:111-116 (1998)
16	oncogenesis	38827_at	anterior gradient 2 homolog (Xenepus laevis)	104	162200_r_at	AV062476	NM_011783	NP_035913	-	A	88.15%	anterior gradient 2 (Xenopus laevis) Putative Ortholog	1	A	1.3	A	0.7	A	Biochem. Biophys. Res. Commun. 251:111-116 (1998)

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
17	others	1230_g_at	cisplatin resistance associated	105	106584_at	AI182881	-	-	-	B	91.87%	expressed sequence AI035308 Putative Ortholog	0.5	A	0.39	A	0.6	A	-
17	others	1230_g_at	cisplatin resistance associated	106	171229_i_at	AV167772	-	-	-	C	91.87%	expressed sequence AI035308 Putative Ortholog	1.2	A	0.71	A	0.7	A	-
17	others	32527_at	adipose specific 2		none								-		-		-		
17	others	32817_at	SEC14 (S. cerevisiae)-like 2		none								-		-		-		
17	others	38151_at	loss of heterozygosity, 11, chromosomal region 2, gene A	107	162559_at	AI837711	-	-	-	B	90.34%	expressed sequence AW551984 Putative Ortholog	1.2	A	1.5	A	1.8	A	-
17	others	38151_at	loss of heterozygosity, 11, chromosomal region 2, gene A	108	168765_at	AV245837	-	-	-	C	90.34%	expressed sequence AW551984 Putative Ortholog	1.2	A	1.2	A	1	A	-
17	others	38803_at	clone 24665 mRNA (neurocalcin delta)	109	111732_at	AA881910	-	-	-	B	100.00%	ESTs Putative Ortholog (highly conserved)	1	P	0.91	P	1	P	-
17	others	38803_at	clone 24665 mRNA (neurocalcin delta)	110	108756_at	AW045893	NM_134094	NP_598855	-	B		expressed sequence AI848120 Curated Ortholog	1.1	P	0.91	P	0.7	P	Unpublished :- (2001)
17	others	38803_at	clone 24665 mRNA (neurocalcin delta)	111	112376_at	AW124163	NM_134094	NP_598855	-	B		expressed sequence AI848120 Curated Ortholog	1.2	A	1	A	2.5	A	Unpublished :- (2001)

Table 70

17	others	38803_at	clone 24665 mRNA (neurocalcin delta)	112	140699_at	AW124014	-	-	-	C	100.00%	ESTs Putative Ortholog (highly conserved)	0.9	A	0.77	A	1.3	A	-
17	others	39827_at	RTP801	113	103460_at	AI849939	-	-	-	A	92.59%	RIKEN cDNA 5830413E08 gene Putative Ortholog (highly conserved)	1	A	1.1	A	1	A	-
17	others	41841_at	GPI-anchored metastasis-associated protein homolog	114	163822_at	AA073823	NM_133743	NP_598504	-	B	85.05%	GPI-anchored metastasis-associated protein homolog Putative Ortholog	1.5	P	0.87	P	1	A	Genome Res. 10:1617-1630 (2000)
17	others	41841_at	GPI-anchored metastasis-associated protein homolog	115	169732_i_at	AV075775	NM_133743	NP_598504	-	C	85.05%	GPI-anchored metastasis-associated protein homolog Putative Ortholog	0.9	A	0.33	A	0.7	A	Genome Res. 10:1617-1630 (2000)

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
18	P450	1371_s_at	cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6	116	102701_at	M21856	-	AAA40425	-	A	86.47%	cytochrome P450, 2b10, phenobarbitol inducible, type b Putative Ortholog (highly conserved)	0.8	P	0.67	P	0.8	P	Biochemistry 27:6434-6443 (1998)
18	P450	1371_s_at	cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6	117	102690_at	AF047529	NM_007814	NP_031840	7 7.3 Cm	A	84.80%	cytochrome P450, 2b19 Homolog	1.6	A	0.42	A	0.6	A	Genomics 53:417-419 (1998)
18	P450	37124_i_at	cytochrome P450, subfamily IIIA, polypeptide 5		none								-		-		-		
18	P450	37125_f_at	cytochrome P450, subfamily IIIA, polypeptide 5		none								-		-		-		

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
19	phosphatase	1005_at	dual specificity phosphatase 1	118	168811_i_at	AV216941	NM_013642	NP_038670	17 13.0 cM	C		protein tyrosine phosphatase, non-receptor type 16 Curated Ortholog	12	A	1.2	A	0.7	A	Oncogene 7:187-190 (1992)
19	phosphatase	1005_at	dual specificity phosphatase 1	119	104598_at	X61940	NM_013642	NP_038670	17 13.0 cM	A	89.18%	protein tyrosine phosphatase, non-receptor type 16 Putative Ortholog (highly conserved)	0.7	P	0.63	P	0.4	P	Oncogene 7:187-190 (1992)
19	phosphatase	1364_at	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	120	92380_r_at	AJ133130	NM_011219	NP_035349	-	A		protein tyrosine phosphatase, receptor type, Z Curated Ortholog	1.3	A	0.77	A	1.4	A	J. Neurosci. 19:3888-3899 (1999)
19	phosphatase	1364_at	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	121	169826_f_at	AV151279	NM_011219	NP_035349	-	C		protein tyrosine phosphatase, receptor type, Z Curated Ortholog	1	A	1.9	A	0.6	A	J. Neurosci. 19:3888-3899 (1999)
19	phosphatase	1364_at	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	122	134749_f_at	AI662731	NM_011219	NP_035349	-	C		protein tyrosine phosphatase, receptor type, Z Curated Ortholog	0.9	A	0.83	A	0.6	A	J. Neurosci. 19:3888-3899 (1999)
19	phosphatase	1364_at	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	123	165782_at	AW120852	-	-	-	C	90.44%	Mus musculus, clone IMAGE:3590815, mRNA, partial cds Putative Ortholog (highly conserved)	0.6	A	0.67	A	1.6	P	-

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
20	protein binding protein	1586_at	insulin-like growth factor binding protein 3	124	95083_at	X81581	NM_008343	NP_032369	11 1.35 cM	A	83.12%	insulin-like growth factor binding protein 3 Putative Ortholog	0.4	A	0.77	A	0.2	A	Mol. Cell. Endocrinol. 104:57-66 (1994)
20	protein binding protein	1586_at	insulin-like growth factor binding protein 3	125	95082_at	AI842277	NM_008343	NP_032369	11 1.35 cM	A	83.12%	insulin-like growth factor binding protein 3 Putative Ortholog	1	P	0.18	M	0.2	M	Mol. Cell. Endocrinol. 104:57-66 (1994)

Table 71

cat#	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASMS 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
20	protein binding protein	37319_at	insulin-like growth factor binding protein 3	124	95083_at	X81581	NM_008343	NP_032369	11 1.35 cM	A	83.12%	insulin-like growth factor binding protein 3 Putative Ortholog	0.4	A	0.77	A	0.2	A	Mol. Cell. Endocrinol. 104:57-66 (1994)
20	protein binding protein	37319_at	insulin-like growth factor binding protein 3	125	95082_at	AI842277	NM_008343	NP_032369	11 1.35 cM	A	83.12%	insulin-like growth factor binding protein 3 Putative Ortholog	1	P	0.18	M	0.2	M	Mol. Cell. Endocrinol. 104:57-66 (1994)
20	protein binding protein	1736_at	insulin-like growth factor binding protein 6	126	103904_at	X81584	NM_008344	NP_032370	-	A	83.27%	insulin-like growth factor binding protein 6 Putative Ortholog (highly conserved)	0.7	P	0.63	P	0.7	P	Mol. Cell. Endocrinol. 104:57-66 (1994)
20	protein binding protein	32149_at	microseminoprotein, beta	127	100715_at	U89840	NM_020597	NP_065622	-	A		beta-microseminoprotein Curated Ortholog	2.1	P	1.1	A	0.9	A	DNA Cell Biol. 18:11-26 (1999)

cat#	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASMS 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
21	proteinase	40717_at	cathepsin L2		none														

cat#	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASMS 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
22	proteinase inhibitor	33305_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin),member 1		-	AK018226	XM_110043	XP_110043	-	-	75.00%	serine (or cysteine) proteinase inhibitor, clade B, member 1b	-		-		-		-
22	proteinase inhibitor	33825_at	serine (or cysteine) proteinase inhibitor, clade A (alpha-1antiproteinase, antitrypsin), member3	128	103811_at	AB012693	NM_010581	NP_034711	-	A	89.81%	integrin-associated protein Putative Ortholog	1	P	1	P	1	P	J. Cell Biol. 123:485-496 (1993)
22	proteinase inhibitor	38125_at	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	129	94147_at	M33960	NM_008871	NP_032897	-	A	91.34%	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 Putative Ortholog (highly conserved)	0.9	P	1.4	P	1	P	Mol. Cell. Biol. 10:1265-1269 (1990)
22	proteinase inhibitor	672_at	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	129	94147_at	M33960	NM_008871	NP_032897	-	A	91.34%	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 Putative Ortholog (highly conserved)	0.9	P	1.4	P	1	P	Mol. Cell. Biol. 10:1265-1269 (1990)
22	proteinase inhibitor	662_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5	130	170241_f_at	AV077498	NM_009257	NP_033283	-	C		serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5 Curated Ortholog	0.5	A	0.39	A	0.7	A	Unpublished :- 0
22	proteinase inhibitor	662_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5	131	100034_at	U54705	NM_009257	NP_033283	-	A	86.74%	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5 Putative Ortholog	0.5	A	0.91	A	1	A	Unpublished :- 0
22	proteinase inhibitor	662_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5	132	165730_at	AI848751	NM_009257	NP_033283	-	C	86.73%	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5 Putative Ortholog	1.6	A	0.77	A	1.2	A	Unpublished :- 0

cat#	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASMS 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
23	S100	41096_at	S100 calcium-binding protein A8	133	101634_at	M33212	NM_008722	NP_032748	-	A	94.83%	nucleophosmin 1 Putative Ortholog (highly conserved)	1.1	P	1	P	1	P	Chromosoma 96:417-426 (1988)
23	S100	41096_at	S100 calcium-binding protein A8	134	103449_at	M83218	NM_013650	NP_038678	3 43.6 cM	A	94.83%	S100 calcium binding protein A8 (calgranulin A) Curated Ortholog	1.5	P	2	P	0.3	P	Blood 79 (8), 1907-1915 (1992)

Table 72

cat#	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_RefSeq	mouse_RefSeqP	mouse_Map Location	chip ID	homology	name	MAS5 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
23	S100	41098_at	S100 calcium-binding protein A8	135	165722_r_at	AV300070	NM_008722	NP_032748	-	C	94.83%	nucleophosmin 1 Putative Ortholog (highly conserved)	1.2	A	0.77	A	0.7	A	Chromosoma 96:417-426 (1988)
23	S100	41098_at	S100 calcium-binding protein A8	136	165723_at	AV285738	NM_008722	NP_032748	-	C	94.83%	nucleophosmin 1 Putative Ortholog (highly conserved)	0.5	A	1.7	A	1.1	A	Chromosoma 96:417-426 (1988)
24	signal transduction	1057_at	Human retinoic acid-binding protein II (CRABP-II) gene exons 2-4	137	137179_at	AI325535	-	-	-	C	89.82%	cellular retinoic acid binding protein II Putative Ortholog (highly conserved)	0.7	A	0.91	A	0.9	A	-
24	signal transduction	1057_at	Human retinoic acid-binding protein II (CRABP-II) gene exons 2-4	138	100127_at	M35523	-	AAA37454	-	A	89.82%	cellular retinoic acid binding protein II Putative Ortholog (highly conserved)	1.7	A	0.44	A	0.5	A	roc. Natl. Acad. Sci. USA. 87:6233-6237 (1990)
24	signal transduction	41783_at	Human retinoic acid-binding protein II (CRABP-II) gene exons 2-4	137	137179_at	AI325535	-	-	-	C	89.82%	cellular retinoic acid binding protein II Putative Ortholog (highly conserved)	0.7	A	0.91	A	0.9	A	-
24	signal transduction	41783_at	Human retinoic acid-binding protein II (CRABP-II) gene exons 2-4	138	100127_at	M35523	-	AAA37454	-	A	89.82%	cellular retinoic acid binding protein II Putative Ortholog (highly conserved)	1.7	A	0.44	A	0.5	A	roc. Natl. Acad. Sci. U.S.A. 87:6233-6237 (1990)
24	signal transduction	35632_at	Cas-Br-M (murine) ectropic retroviral transforming sequence b	139	110236_at	AI430283	-	-	-	B	93.58%	expressed sequence AI429560 Putative Ortholog (highly conserved)	1.1	P	1.3	P	0.9	P	-
24	signal transduction	514_at	Cas-Br-M (murine) ectropic retroviral transforming sequence b	139	110236_at	AI430283	-	-	-	B	93.58%	ESTs Putative Ortholog (highly conserved)	1.1	P	1.3	P	0.9	P	-
24	signal transduction	38524_at	Rho guanine nucleotide exchange factor 4, isoform a NM_032995 Rho guanine nucleotide exchange factor 4, isoform b	140	165779_i_at	AW124292	-	-	-	C	92.34%	ESTs, Weakly similar to VAV3_MOUSE VAV-3 PROTEIN [M.musculus] Putative Ortholog (highly conserved)	0.8	A	0.91	A	1.8	A	-
24	signal transduction	39220_at	uteroglobin	141	94291_at	L04503	NM_011681	NP_035811	-	A		uteroglobin Curated Ortholog	1	P	1	P	1.1	P	Exp. Lung Res. 19:67-75 (1993)
24	signal transduction	1778_g_at	ras inhibitor	142	109308_at	AI303500	-	-	-	B	85.96%	Mus musculus, clone MGC:12160 IMAGE:3711198, mRNA, complete cds Putative Ortholog	1.3	A	1.1	A	1.5	A	-
24	signal transduction	1934_s_at	vascular endothelial growth factor C	143	94712_at	U73620	NM_009506	NP_033532	8	A	86.20%	vascular endothelial growth factor C Homolog	0.5	A	0.91	A	0.7	A	Development 122:3829-3837 (1996)
24	signal transduction	32737_at	ras-related C3 botulinum toxin substrate 2	144	103579_at	X53247	NM_009008	NP_033034	-	A	92.88%	RAS-related C3 botulinum substrate 2 Curated Ortholog	1.2	P	1.3	P	1	P	Oncogene 5:769-772 (1990)
25	structural protein	34091_s_at	vimentin	145	101046_at	X56397	NM_011701	NP_035831	2 7.0 cM	A		vimentin Curated Ortholog	1	A	0.77	A	0.9	A	Gene 78:171-175 (1989)
25	structural protein	34091_s_at	vimentin	146	162379_r_at	AV245272	NM_011701	NP_035831	2 7.0 cM	A		vimentin Curated Ortholog	0.9	A	1	P	0.7	A	Gene 78:171-175 (1989)
25	structural protein	38113_s_at	troponin T1, skeletal, slow	147	161361_s_at	AV213431	NM_011618	NP_035748	7 9.0 cM	A	89.53%	troponin T1, skeletal, slow Putative Ortholog (highly conserved)	1.8	A	0.35	A	1.3	A	Gene 214:1-2 (1998)
25	structural protein	38113_s_at	troponin T1, skeletal, slow	148	101383_at	AJ131711	NM_011618	NP_035748	7 9.0 cM	A	89.53%	troponin T1, skeletal, slow Putative Ortholog (highly conserved)	1.3	P	1.2	A	1	P	Gene 214:1-2 (1998)
25	structural protein	36355_at	involucrin	149	92739_at	L28819	NM_008412	NP_032438	3 45.2 cM	A		involucrin Curated Ortholog	1.2	A	0.81	A	0.7	A	Mol. Biol. Evol. 10:1136-1149 (1993)
25	structural protein	38790_at	tropomyosin 1 (alpha)	150	113786_at	AI314966	NM_024427	NP_077745	9 40.0 cM	B		tropomyosin 1, alpha Curated Ortholog	0.8	A	1.2	P	1.4	P	Mol. Cell. Biol. 8:5561-5565 (1988)

Table 73

25	structural protein	36790_at	tropomyosin 1 (alpha)	151	105003_at	AA939874	NM_024427	NP_077745	9 40.0 cM	B		tropomyosin 1, alpha Curated Ortholog	1	A	0.67	A	0.6	A	Mol. Cell. Biol. 8:5561-5565 (1988)
25	structural protein	36790_at	tropomyosin 1 (alpha)	152	160532_at	M22479	NM_024427	NP_077745	9 40.0 cM	A		tropomyosin 1, alpha Curated Ortholog	1	P	1	P	1	P	Mol. Cell. Biol. 8:5561-5565 (1988)
25	structural protein	36791_g_at	tropomyosin 1 (alpha)	150	113796_at	AI314988	NM_024427	NP_077745	9 40.0 cM	B		tropomyosin 1, alpha Curated Ortholog	0.8	A	1.2	P	1.4	P	Mol. Cell. Biol. 8:5561-5565 (1988)
25	structural protein	36791_g_at	tropomyosin 1 (alpha)	151	105003_at	AA939874	NM_024427	NP_077745	9 40.0 cM	B		tropomyosin 1, alpha Curated Ortholog	1	A	0.67	A	0.6	A	Mol. Cell. Biol. 8:5561-5565 (1988)
25	structural protein	36791_g_at	tropomyosin 1 (alpha)	152	160532_at	M22479	NM_024427	NP_077745	9 40.0 cM	A		tropomyosin 1, alpha Curated Ortholog	1	P	1	P	1	P	Mol. Cell. Biol. 8:5561-5565 (1988)
25	structural protein	36792_at	tropomyosin 1 (alpha)	150	113796_at	AI314988	NM_024427	NP_077745	9 40.0 cM	B		tropomyosin 1, alpha Curated Ortholog	0.8	A	1.2	P	1.4	P	Mol. Cell. Biol. 8:5561-5565 (1988)
25	structural protein	36792_at	tropomyosin 1 (alpha)	151	105003_at	AA939874	NM_024427	NP_077745	9 40.0 cM	B		tropomyosin 1, alpha Curated Ortholog	1	A	0.67	A	0.6	A	Mol. Cell. Biol. 8:5561-5565 (1988)
25	structural protein	36792_at	tropomyosin 1 (alpha)	152	160532_at	M22479	NM_024427	NP_077745	9 40.0 cM	A		tropomyosin 1, alpha Curated Ortholog	1	P	1	P	1	P	Mol. Cell. Biol. 8:5561-5565 (1988)
25	structural protein	37160_at	small proline-rich protein 1B (cornifin)	153	100446_r_at	X91825	NM_009265	NP_033291	3 45.2 cM	A		small proline-rich protein 1B Curated Ortholog	1	P	0.83	P	1	P	J. Invest. Dermatol. 106:294-304 (1996)
25	structural protein	37160_at	small proline-rich protein 1B (cornifin)	154	100445_f_at	X91825	NM_009265	NP_033291	3 45.2 cM	A		small proline-rich protein 1B Homolog	2.2	A	0.3	A	0.9	A	J. Invest. Dermatol. 106:294-304 (1996)
25	structural protein	37160_at	small proline-rich protein 1B (cornifin)	155	164832_i_at	AV225959	-	-	-	B		RIKEN cDNA C530009C10 gene Putative Ortholog	0.6	A	2.2	A	1	A	-
25	structural protein	37582_at	keratin 15	156	160852_at	D16313	NM_008469	NP_032495	11 59.5 cM	A		keratin complex 1, acidic, gene 15 Curated Ortholog	1.8	A	0.83	A	1.1	A	Gene 138:1-2 (1994)
25	structural protein	37582_at	keratin 15	157	164618_f_at	AV171812	NM_008469	NP_032495	11 58.5 cM	B		keratin complex 1, acidic, gene 15 Curated Ortholog	1.6	P	0.67	P	0.8	P	Gene 138:1-2 (1994)
25	structural protein	39569_at	envoplakin	158	163295_at	AI561819	NM_025276	NP_079552	-	B		envoplakin Curated Ortholog	1.4	A	0.83	A	1.7	A	Meth. Enzymol. 303:19-44 (1999)

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
26	transcription factor	1452_at	LIM domain only 4	159	98122_at	AF074600	NM_010723	NP_034853	73.1 cM	A	95.77%	LIM only 4 Putative Ortholog (highly conserved)	1.2	P	1.3	P	1.3	P	Proc. Natl. Acad. Sci. U.S.A. 95:11257-11262 (1998)
26	transcription factor	33439_at	ion factor 8 (represses interleukin 2 expression)	160	99052_at	D76432	NM_011546	NP_035676	18 0.0 cM	A	95.71%	zinc finger homeobox 1a Putative Ortholog	1	P	0.77	P	0.7	P	Gene 169:289-290 (1996)
26	transcription factor	34216_at	Kruppel-like factor 7 (ubiquitous)	161	104645_at	AI853712	NM_033563	NP_291041	1C1-C3	A	94.84%	Kruppel-like factor 7 (ubiquitous) Putative Ortholog (highly conserved)	1	P	0.77	P	0.6	P	Unpublished :- ()
26	transcription factor	34216_at	Kruppel-like factor 7 (ubiquitous)	162	112898_at	AW045878	NM_033563	NP_291041	1C1-C3	B	94.84%	Kruppel-like factor 7 (ubiquitous) Putative Ortholog (highly conserved)	1.3	P	1	P	1.2	P	Unpublished :- ()
26	transcription factor	34216_at	Kruppel-like factor 7 (ubiquitous)	163	107020_at	AW049268	NM_033563	NP_291041	1C1-C3	B	94.84%	Kruppel-like factor 7 (ubiquitous) Putative Ortholog (highly conserved)	0.7	P	1.1	A	0.9	A	Unpublished :- ()
26	transcription factor	34216_at	Kruppel-like factor 7 (ubiquitous)	164	114908_at	AI648497	NM_033563	NP_291041	1C1-C3	B	94.84%	Kruppel-like factor 7 (ubiquitous) Putative Ortholog (highly conserved)	0.7	P	1.1	P	0.7	P	Unpublished :- ()
26	transcription factor	35425_at	BarH-like homeobox 2	165	100738_at	L77800	NM_013800	NP_038828	-	A	93.70%	BarH-like homeobox 2 Putative Ortholog	0.4	A	0.59	A	0.5	A	Proc. Natl. Acad. Sci. U.S.A. 94:2632-2637 (1997)
26	transcription factor	36619_r_at	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	166	100050_at	M31885	-	AAA37879	-	A		inhibitor of DNA binding 1 Curated Ortholog	0.9	P	0.71	P	0.7	P	Cell 61:49-59 (1990)

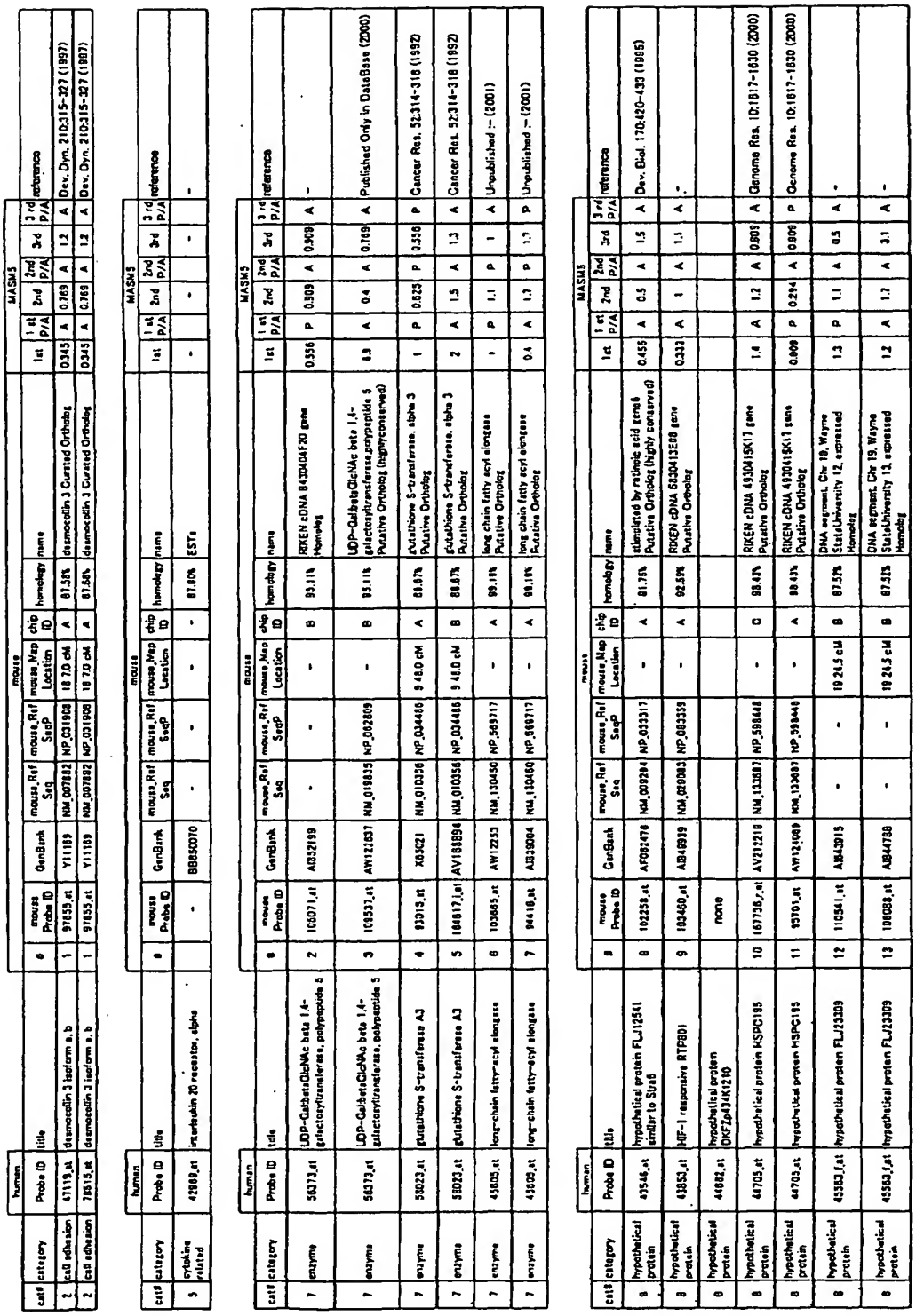
Table 74

cat#	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
26	transcription factor	41246_at	DKFZP586I1024 protein	187	97487_at	X70296	NM_009255	NP_033281	1 48.5 Cm	A	91.81%	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 Putative Ortholog	1.2	A	1.1	A	1.3	A	EMBO J. 12:1871-1878 (1993)

cat#	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
27	transporter	1932_at	ATP-binding cassette, sub-family C, member 5	168	103600_at	AB019003	NM_013790	NP_038818	16 14.0 cM	A	90.79%	ATP-binding cassette, sub-family C, member 5a	0.8	A	1	A	1	P	Biochim. Biophys. Acta. 1461:347-357 (1999)
27	transporter	1932_at	ATP-binding cassette, sub-family C, member 5	169	165744_at	AW124768	NM_013790	NP_038818	16 14.0 cM	C	98.08%	ATP-binding cassette, sub-family C (CFTR/MRP), member 5a Curated Ortholog	0.8	A	1.5	A	1.2	A	Biochim. Biophys. Acta. 1461:347-357 (1999)
27	transporter	1932_at	ATP-binding cassette, sub-family C, member 5	170	169447_r_at	AV168159	NM_013790	NP_038818	16 14.0 cM	C		ATP-binding cassette, sub-family C (CFTR/MRP), member 5a Curated Ortholog	3.1	A	3	A	0.4	A	Biochim. Biophys. Acta. 1461:347-357 (1999)
27	transporter	32531_at	connexin 43	171	100064_f_at	M63801	NM_010288	NP_034418	10 28.0 cM	A		gap junction membrane channel protein alpha 1 Curated Ortholog.	1.1	P	1.4	P	1.1	P	J. Biol. Chem. 266:7971-7974 (1991)
27	transporter	32531_at	connexin 43	172	100065_r_at	M63801	NM_010288	NP_034418	10 28.0 cM	A		gap junction membrane channel protein alpha 1 Curated Ortholog	1.2	P	0.81	P	0.9	P	J. Biol. Chem. 266:7971-7974 (1991)
27	transporter	32809_at	Aquaporin-5	173	113916_at	AI182792	NM_009701	NP_033831	15 58.8 cM	B		aquaporin 5 Curated Ortholog	0.8	P	0.83	P	0.6	P	Mamm. Genome 10:498-505 (1999)
27	transporter	37591_at	uncoupling protein 2	174	92792_at	U69135	NM_011671	NP_035801	7 50.0 cM	A	91.28%	uncoupling protein 2, mitochondrial Homolog	1.5	A	1.3	A	0.8	A	Diabetes 46:900-906(1997)
27	transporter	39682_at	sodium channel, nonvoltage-gated 1, beta	175	110692_at	AI508632	NM_011325	NP_035455	7 56.0 cM	B	87.58%	sodium channel, nonvoltage-gated 1 beta Putative Ortholog (highly conserved)	0.4	P	0.38	A	0.2	A	Am. J. Physiol. 277:- (1999)
27	transporter	40297_at	six transmembrane epithelial antigen of the prostate		-	AK010437	NM_027399	NP_081675	5 3.0 cM	-	81.00%	six transmembrane epithelial antigen of the prostate	-		-		-		Nature 409 (6821), 685-690 (2001)
27	transporter	40339_at	gamma-aminobutyric acid (GABA) A receptor	176	163918_at	AV216203	-	-	-	B	88.69%	Mus musculus, clone MGC:28005 IMAGE:3602400, mRNA, complete cds Putative Ortholog (highly conserved)	1.2	P	1.5	P	1	P	-
27	transporter	40339_at	gamma-aminobutyric acid (GABA) A receptor	177	169112_r_at	AV216203	-	-	-	C	88.69%	Mus musculus, clone MGC:28005 IMAGE:3602400, mRNA, complete cds Putative Ortholog (highly conserved)	1.4	A	1.4	A	1	A	-

cat#	category	human Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MASM5 1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
		33548_at	clone=IMAGE-2448791		none														
		38252_at	clone 23620 mRNA	178	140497_at	AW124202	-	-	-	C	83.44%	ESTs Putative Ortholog (highly conserved)	0.8	P	0.77	P	1.8	P	-
		40191_s_at	clone IMAGE 21721	179	131152_at	AW142707	-	-	-	C	89.92%	Mus musculus, Similar to KIAA0582 protein, clone MGC:6990 IMAGE:3154964, mRNA, complete cds Putative Ortholog	0.8	A	0.71	A	0.8	A	-

Table 75



cat#	category	human Probe ID	human title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MAS#5 1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
2	cell adhesion	47119_at	desmocollin 3 isoform a, b	1	97655_at	Y11189	NM_007882	NP_031908	18 7.0 cM	A	87.38%	desmocollin 3 Curated Ortholog	0.345	A	0.769	A	1.2	A	Dev. Dyn. 210:315-327 (1997)
2	cell adhesion	78519_at	desmocollin 3 isoform a, b	1	97655_at	Y11189	NM_007882	NP_031908	18 7.0 cM	A	87.86%	desmocollin 3 Curated Ortholog	0.345	A	0.769	A	1.2	A	Dev. Dyn. 210:315-327 (1997)

cat#	category	human Probe ID	human title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MAS#5 1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
5	cytokine related	42988_at	interleukin 20 receptor, alpha		-	BB650070	-	-	-	-	87.80%	ESTs	-		-		-		-

cat#	category	human Probe ID	human title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MAS#5 1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
7	enzyme	56373_at	UDP-GalNAc:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	2	106071_at	AI852199	-	-	-	B	93.11%	RIKEN cDNA B430104F20 gene Homolog	0.356	P	0.909	A	0.909	A	-
7	enzyme	56373_at	UDP-GalNAc:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	3	109537_at	AW121637	NM_019835	NP_062809	-	B	93.11%	UDP-GalNAc:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5 Putative Ortholog (highly conserved)	0.8	A	0.4	A	0.769	A	Published Only in DataBase (2000)
7	enzyme	58023_at	glutathione S-transferase A3	4	93013_at	X65021	NM_010356	NP_034486	9 48.0 cM	A	88.67%	glutathione S-transferase, alpha 3 Putative Ortholog	1	P	0.823	P	0.556	P	Cancer Res. 52:314-318 (1992)
7	enzyme	58023_at	glutathione S-transferase A3	5	106617_at	AV108894	NM_010356	NP_034486	9 48.0 cM	B	88.67%	glutathione S-transferase, alpha 3 Putative Ortholog	2	A	1.5	A	1.3	A	Cancer Res. 52:314-318 (1992)
7	enzyme	45805_at	long-chain fatty-acyl elongase	6	103665_at	AW12253	NM_130450	NP_569717	-	A	93.11%	long chain fatty acyl elongase Putative Ortholog	1	P	1.1	P	1	A	Unpublished -- (2001)
7	enzyme	45805_at	long-chain fatty-acyl elongase	7	94418_at	AI839004	NM_130460	NP_569717	-	A	93.11%	long chain fatty acyl elongase Putative Ortholog	0.4	A	1.7	P	1.7	P	Unpublished -- (2001)

cat#	category	human Probe ID	human title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	MAS#5 1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
8	hypothetical protein	47546_at	hypothetical protein FLJ12541 similar to Sin6	8	102258_at	AF081478	NM_009284	NP_033317	-	A	81.78%	stimulated by retinoic acid gene6 Putative Ortholog (highly conserved)	0.455	A	0.5	A	1.5	A	Dev. Biol. 170:420-433 (1995)
8	hypothetical protein	43853_at	NIF-1 responsive RTP801	9	103460_at	AB049939	NM_019083	NP_063359	-	A	92.59%	RIKEN cDNA 6330413E08 gene Putative Ortholog	0.333	A	1	A	1.1	A	-
8	hypothetical protein	44682_at	hypothetical protein DKFZp434K1210		none														
8	hypothetical protein	44705_at	hypothetical protein HSPC185	10	107738_at	AV212218	NM_133687	NP_598448	-	C	98.43%	RIKEN cDNA 4930415K17 gene Putative Ortholog	1.4	A	1.2	A	0.909	A	Genome Res. 10:1817-1830 (2000)
8	hypothetical protein	44705_at	hypothetical protein HSPC185	11	95701_at	AW124069	NM_133687	NP_598448	-	A	98.43%	RIKEN cDNA 4930415K17 gene Putative Ortholog	0.909	P	0.294	A	0.909	P	Genome Res. 10:1817-1830 (2000)
8	hypothetical protein	45363_at	hypothetical protein FLJ23309	12	110541_at	AI843915	-	-	19 24.5 cM	B	87.57%	DNA segment, Chr 19, Wayne StateUniversity 12, expressed Homolog	1.3	P	1.1	A	0.5	A	-
8	hypothetical protein	45363_at	hypothetical protein FLJ23309	13	106028_at	AI844788	-	-	19 24.5 cM	B	87.57%	DNA segment, Chr 19, Wayne StateUniversity 12, expressed Homolog	1.2	A	1.7	A	3.1	A	-

Table 76

		human		mouse									MASMS						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
8	hypothetical protein	46924_at	hypothetical protein MGC12538	14	165731_at	AV204598	-	-	-	C	88.24%	RIKEN cDNA 2310005O05 gene Putative Ortholog	1.8	A	1.7	A	0.5	A	-
8	hypothetical protein	47534_at	hypothetical protein FLJ23516	15	162582_at	AI840292	NM_023270	NP_075759	-	B	94.29%	RIKEN cDNA 1300002C13 gene Putative Ortholog (highly conserved)	2	A	1.8	A	2	A	Genome Res. 10:1617-1630 (2000)
8	hypothetical protein	47534_at	hypothetical protein FLJ23516	16	108010_at	AW210455	NM_023270	NP_075759	-	B	94.29%	RIKEN cDNA 1300002C13 gene Putative Ortholog (highly conserved)	1.2	P	2.2	P	1.4	A	Genome Res. 10:1617-1630 (2000)
8	hypothetical protein	52012_at	hypothetical protein FLJ10718		none														
8	hypothetical protein	54030_at	hypothetical protein FLJ20373		-	AW046177	-	-	-		84.20%	expressed sequence AW046177	-		-		-		-
8	hypothetical protein	55924_at	hypothetical protein MGC14128		none								-		-		-		
8	hypothetical protein	51669_r_at	hypothetical protein MGC14128		none								-		-		-		
8	hypothetical protein	57777_at	hypothetical protein PRO1489	17	162963_at	AI835402	-	-	-	B	92.56%	expressed sequence AI831706 Putative Ortholog	0.887	P	0.528	P	0.887	P	-
8	hypothetical protein	42473_at	Homo sapiens cDNA FLJ11971 fis, clone HEMBB1001208		none								-		-		-		
8	hypothetical protein	43412_s_at	hypothetical protein MGC16207		none														
8	hypothetical protein	48104_at	Homo sapiens mRNA; cDNA DKFZp434H1235 (from clone DKFZp434H1235); partial cds	18	116700_at	AI314284	NM_025807	NP_080083	-	B	91.77%	RIKEN cDNA 1200003C15 gene Putative Ortholog (highly conserved)	1.3	P	1.1	P	1.1	P	-
8	hypothetical protein	46293_at	Homo sapiens cDNA FLJ31097 fis, clone IMR321000210		-	AK003761	NM_028841	NP_083117	-	-		RIKEN cDNA 2210021G21	-		-		-		Meth. Enzymol. 303, 19-44 (1999)
8	hypothetical protein	46700_at	Homo sapiens mRNA; cDNA DKFZp586E1624 (from clone DKFZp586E1624)		none								-		-		-		
8	hypothetical protein	47432_at	prostate cancer associated protein 1	19	106880_at	AW121537	-	-	-	B	88.00%	expressed sequence AW045835 Putative Ortholog	1.1	A	1.2	A	1.2	A	-
8	hypothetical protein	48088_at	Homo sapiens cDNA FLJ30086 fis, clone BNGH41000002, moderately similar to ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (EC 6.3.4.4)	20	102018_at	AI854879	-	-	-	A	98.00%	RIKEN cDNA 1500001K17 gene Putative	1	P	1.1	P	1	P	-
8	hypothetical protein	48539_at	Homo sapiens cDNA: FLJ22539 fis, clone HRC13227		none														
8	hypothetical protein	52634_at	Homo sapiens mRNA; cDNA DKFZp434H1235 (from clone DKFZp434H1235); partial cds	21	115700_at	AI314284	NM_025807	NP_080083	-	B	84.14%	RIKEN cDNA 1200003C15 gene PutativeOrtholog (highly conserved)	1.3	P	1.1	P	1.1	P	-
8	hypothetical protein	52637_g_at	Homo sapiens mRNA; cDNA DKFZp434H1235 (from clone DKFZp434H1235); partial cds	21	115700_at	AI314284	NM_025807	NP_080083	-	B	84.14%	RIKEN cDNA 1200003C15 gene Putative Ortholog (highly conserved)	1.3	P	1.1	P	1.1	P	-
8	hypothetical protein	58531_g_at	KIAA1547 protein		-	X73360	-	CAA51770	-	-	97.00%	EGS protein	-		-		-		Eur. J. Biochem. 216 (1), 343-352 (1993)
8	hypothetical protein	59138_at	Homo sapiens cDNA FLJ30761 fis, clone FEBRA2000538		none								-		-		-		

Table 77

10	kinase	50075_at	chromosome 1 open reading frame 28	22	98370_at	AV381278	-	-	-	A	98.44%	expressed sequence C81219 Putative Ortholog	2.5	P	0.833	A	1	A	-
10	kinase	50075_at	chromosome 1 open reading frame 28	23	111191_at	AW120521	-	-	-	B	98.44%	expressed sequence C81220 Putative Ortholog	5.2	A	0.357	A	2.8	A	-

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
11	matrix protein	52578_s_at	spondin 2, extracellular matrix protein		none														

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP.	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
12	membrane protein	44783_s_at	hairy/enhancer-of-split related with YRPW motif 1	24	101913_at	AW214298	NM_010423	NP_034553	3 24 cM	A	89.52%	hairy/enhancer-of-split related with YRPW motif 1 Putative Ortholog (highly conserved)	1	M	1.3	A	1.2	P	Biochem. Biophys. Res. Commun. 260:459-465 (1999)
12	membrane protein	44783_s_at	hairy/enhancer-of-split related with YRPW motif 1	25	170560_r_at	AV333303	NM_010423	NP_034553	3 24 cM	C	89.52%	hairy/enhancer-of-split related with YRPW motif 1 Putative Ortholog (highly conserved)	1.5	P	2.3	P	0.909	A	Biochem. Biophys. Res. Commun. 260:459-465 (1999)
12	membrane protein	44783_s_at	hairy/enhancer-of-split related with YRPW motif 1	26	161451_r_at	AV292193	NM_010423	NP_034553	3 24 cM	A	89.52%	hairy/enhancer-of-split related with YRPW motif 1 Putative Ortholog (highly conserved)	0.909	A	1	A	1.1	P	Biochem. Biophys. Res. Commun. 260:459-465 (1999)
12	membrane protein	44783_s_at	hairy/enhancer-of-split related with YRPW motif 1	27	95671_at	AJ243895	NM_010423	NP_034553	3 24 cM	A	89.52%	hairy/enhancer-of-split related with YRPW motif 1 Putative Ortholog (highly conserved)	1	P	1	P	0.769	P	Biochem. Biophys. Res. Commun. 260:459-465 (1999)

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
16	oncogenesis	46200_at	putative cytokine high in normal-1		none								-		-		-		

		human		mouse									MASM5						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
17	others	42065_at	hypothetical protein BC016005		none														
17	others	68288_at	hypothetical protein BC016005		none														
17	others	43849_s_at	hypothetical protein BC015359	28	94370_at	AA615075	-	-	-	A	84.62%	similar to putative,clone MGC:37804 IMAGE:4989150 Putative Ortholog	0.455	A	3.2	A	4.8	A	-
17	others	45394_s_at	hypothetical protein BC015359	28	94370_at	AA615075	-	-	-	A	88.52%	ESTs, Highly similar to OIT1 MOUSE ONCOPROTEININDUCED PROTEIN 1 [M.musculus] Putative Ortholog	0.455	A	3.2	A	4.6	A	-
17	others	46030_at	von Ebner minor salivary gland protein	29	160446_at	U46068	-	AAA87581	2; D2Mit19n and D2Mit25n	A	84.30%	Mus musculus von Ebner minor salivarygland protein mRNA, complete cds Putative Ortholog	1.6	P	3.7	P	3.5	P	J. Biol. Chem. 274:13698-13703 (1999)
17	others	46030_at	von Ebner minor salivary gland protein	30	171144_i_at	AV087463	-	-	-	C	84.30%	Mus musculus von Ebner minor salivarygland protein mRNA, complete cds Putative Ortholog	0.909	A	0.556	A	0.833	A	-

Table 78

17	others	46030_at	von Ebner minor salivary gland protein	31	168855_i_at	AV092579	-	-	-	C	84.30%	Mus musculus von Ebner minor salivarygland protein mRNA, complete cds Putative Ortholog	1.3	A	1.1	A	0.714	A	-
17	others	46030_at	von Ebner minor salivary gland protein	32	169748_at	AV090196	-	-	-	C	84.30%	Mus musculus von Ebner minor salivarygland protein mRNA, complete cds Putative Ortholog	0.833	A	0.909	A	1.3	A	-
17	others	49910_at	LUNX protein; PLUNC (palate lung and nasal epithelium clone); tracheal epithelium enriched protein		-	AI845714	NM_011126	NP_035256	2 H1	-	88.24%	palate, lung, and nasal epithelium expressed transcript Putative Ortholog	1.2	P	1	P	1	P	J. Biol. Chem. 274 (19), 13698-13703 (1999)

	human		mouse										MASMS						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
20	protein binding protein	46271_at	FK506-binding protein 5	33	94297_at	U16959	NM_010220	NP_034350	17 13.0 cM	A		FK506 binding protein 5 (51 kDa) Curated Ortholog	0.244	P	2	P	4.4	P	Mol. Cell. Biol. 15:4395-4402 (1995)
20	protein binding protein	54152_at	eukaryotic translation initiation factor 4E binding protein 1	34	100538_at	U28656	NM_007918	NP_031944	8 80 cM	A		eukaryotic translation initiation factor 4E binding protein 1 Curated Ortholog	0.833	P	1.1	P	0.909	P	J. Biol. Chem 270:18531-18538 (1995)

	human		mouse										MASMS						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
25	structural protein	44730_at	collagen, type XII, alpha 1	35	92313_at	AB844068	NM_007730	NP_031756	9 43.0 cM	A		procollagen, type XII, alpha 1 Curated Ortholog	0.4	A	2	A	0.526	A	Genomics 14:225-231 (1992)
25	structural protein	44730_at	collagen, type XII, alpha 1	36	92314_at	U25652	NM_007730	NP_031756	9 43.0 cM	A		procollagen, type XII, alpha 1 Curated Ortholog	1.2	A	1	A	1.4	A	Genomics 14:225-231 (1992)

	human		mouse										MASMS						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference
27	transporter	45826_at	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3	37	109069_at	AI255382	NM_016917	NP_058613	1 B	B	92.03%	solute carrier family 39 (iron-regulatedtransporter), member 1 Putative Ortholog(highly conserved)	1.2	P	0.714	P	0.714	P	Mol. Cell 5:299-309 (2000)
27	transporter	47575_g_at	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	38	97759_at	U09383	NM_010610	NP_034740	14 A3	A		potassium large conductance calcium-activatedchannel, subfamily M, alpha member 1 Curated Ortholog	2	A	2	P	1	A	Science 261:221-224 (1993)
27	transporter	53798_at	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	38	97759_at	U09383	NM_010610	NP_034740	14 A3	A		potassium large conductance calcium-activatedchannel, subfamily M, alpha member 1 Curated Ortholog	2	A	2	P	1	A	Science 261:221-224 (1993)
27	transporter	48048_at	solute carrier family 34 (sodium phosphate), member 2	39	98994_at	AF081499	NM_011402	NP_035532	-	A		solute carrier family 34 (sodium phosphate), member 2 Curated Ortholog	1.1	P	1.1	P	1	P	Proc. Natl. Acad. Sci. U.S.A. 95:14564-14569 (1998)
27	transporter	51261_at	SAC2 suppressor of actin mutations 2-like (yeast)		none														

	human		mouse										MASMS						
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1st P/A	2nd	2nd P/A	3rd	3rd P/A	reference

Table 79

		44876_at	ESTs, Weakly similar to AF126780 1 retinal short-chain dehydrogenase/reductase retSDR2 [H.sapiens]		none														
		45684_at	ESTs		none								-		-		-		
		46709_at	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	40	94637_at	X85992	-	CAA59984	-	A	83.42%	sema domain, immunoglobulin domain(Ig), transmembrane domain (TM) and shortcytoplasmic domain, (semaphorin) 4B Homolog	1.9	P	1	P	1	M	Neuron 14:941-948 (1995)
		47578_at	ESTs		none								-		-		-		
		48999_at	ESTs		none								-		-		-		
		49819_at	ESTs		none								-		-		-		
		49985_at	ESTs	41	114451_at	AI848332	-	-	-	B	91.29%	ESTs Putative Ortholog (highly conserved)	0.909	P	1.1	P	0.833	P	-
		52384_s_at	ESTs, Weakly similar to guanine nucleotide regulatory protein [H.sapiens]	42	93178_at	AW050346	-	-	-	A	93.17%	neuronal guanine nucleotide exchangefactor Putative Ortholog	0.833	A	1	A	0.476	A	-
		53747_at	ESTs, Moderately similar to 2109260A B cell growth factor [H.sapiens]		none								-		-		-		
		57282_at	ESTs		none								-		-		-		
		88528_s_at	ESTs, Highly similar to fring [Homo sapiens] [H.sapiens]	43	98220_at	AW123157	-	-	11 48.0 cM	A	87.19%	DNA segment, Chr 11, Wayne State University 78, expressed Putative Ortholog (highly conserved)	1	P	1	P	0.833	P	-
		59109_at	ESTs	44	160970_at	AW261569	-	-	-	A	91.35%	ESTs Putative Ortholog (highly conserved)	2.4	A	0.288	A	0.628	A	-
		59567_at	ESTs		none								-		-		-		
		49486_at	ESTs	45	108954_at	AW060538	NM_025980	NP_080256	2 A3	B	94.80%	RIKEN cDNA 2700054M22 gene Putative Ortholog	0.909	P	0.909	P	0.833	A	Meth. Enzymol. 303:19-44 (1999)
		49486_at	ESTs	46	164706_at	AV022728	NM_025980	NP_080256	2 A3	B	94.80%	RIKEN cDNA 2700054M22 gene Putative Ortholog	0.825		1.4		1.8		Meth. Enzymol. 303:19-44 (1999)
		42720_at	ESTs		none								-		-		-		
		55436_at	Homo sapiens, clone IMAGE:4818112, mRNA	47	170083_r_at	AV338868	-	-	-	C	95.58%	ESTs Putative Ortholog	2	P	0.769	A	1.8	A	-
		55436_at	ESTs	48	117308_at	AW120879	-	-	-	B	95.68%	ESTs Putative Ortholog	1.4	A	0.833	A	0.909	A	-
		55436_at	ESTs	49	170414_i_at	AV333824	-	-	-	C	95.68%	ESTs Putative Ortholog	0.714	A	0.833	A	1	A	-
		55436_at	ESTs	50	105944_at	AI844171	-	-	-	B	55.58%	ESTs Putative Ortholog	0.476	A	0.833	A	0.833	A	-
		42769_at	ESTs		none								-		-		-		

Table 80

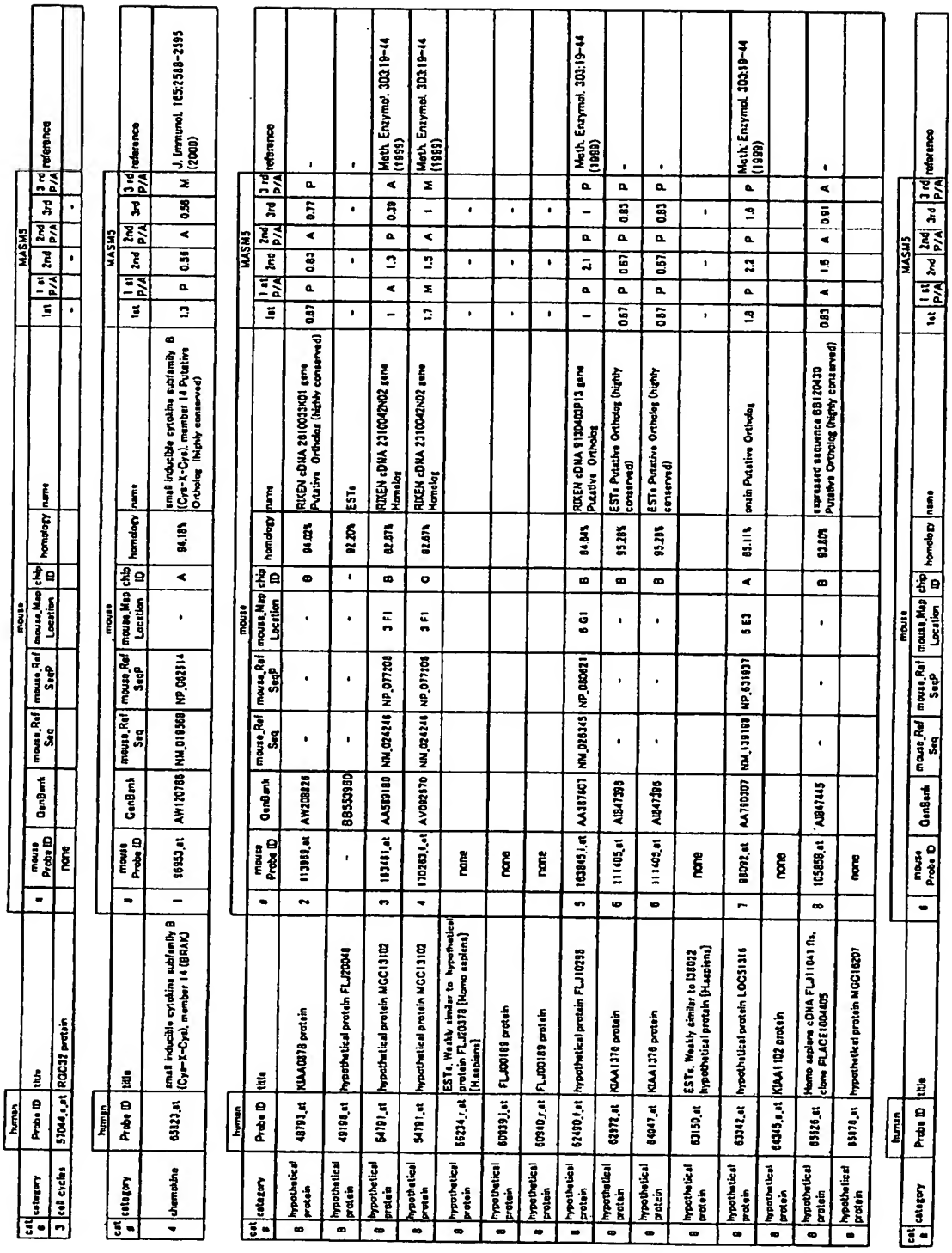


Table 81

cat #	category	human Probe ID	human title	#	mouse Probe ID	mouse GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	mouse chip ID	mouse homology	mouse name	MASM5 1st	MASM5 1st P/A	MASM5 2nd	MASM5 2nd P/A	MASM5 3rd	MASM5 3rd P/A	reference
10	kinase	61873_at	glycerol kinase	9	97525_at	U48403	NM_008194	NP_032220	X 33.0 cM	A	92.70%	glycerol kinase Putative Ortholog (highly conserved)	0.6	A	0.6	A	1.7	A	Genomics 36:530-534 (1996)
10	kinase	61873_at	glycerol kinase	10	169383_r_at	AV037577	NM_008194	NP_032220	X 33.0 cM	C	92.70%	glycerol kinase Curated Ortholog	1.4	A	1	A	1	A	Genomics 36:530-534 (1996)

cat #	category	human Probe ID	human title	#	mouse Probe ID	mouse GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	mouse chip ID	mouse homology	mouse name	MASM5 1st	MASM5 1st P/A	MASM5 2nd	MASM5 2nd P/A	MASM5 3rd	MASM5 3rd P/A	reference
12	membrane protein	63958_at	prostate stem cell antigen	11	160503_at	AW209488	-	-	5 53.0 cM	A	80.69%	prostate stem cell antigen Curated Ortholog	1	A	0.7	A	1.3	A	-

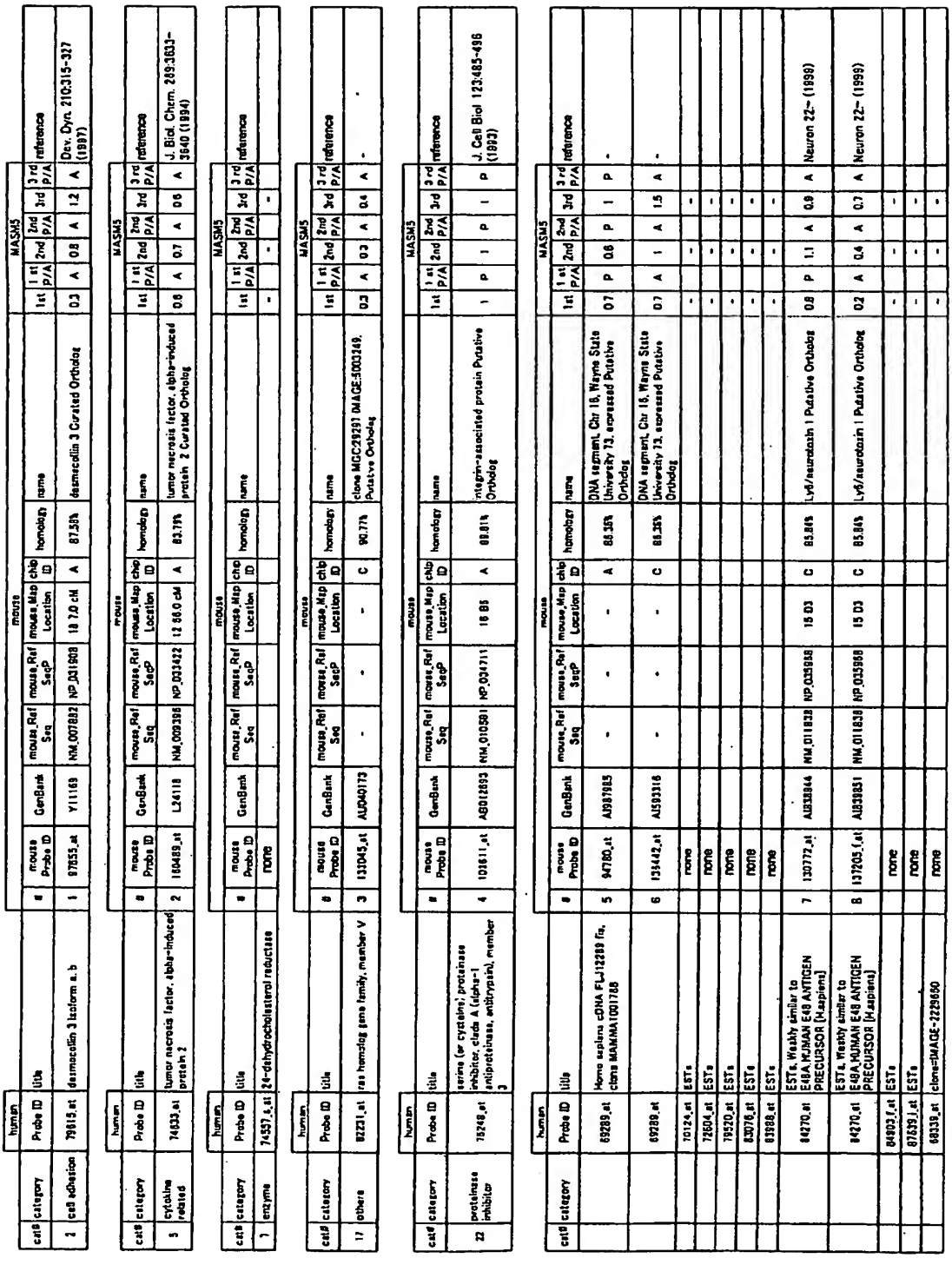
cat #	category	human Probe ID	human title	#	mouse Probe ID	mouse GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	mouse chip ID	mouse homology	mouse name	MASM5 1st	MASM5 1st P/A	MASM5 2nd	MASM5 2nd P/A	MASM5 3rd	MASM5 3rd P/A	reference
17	others	55440_at	palate, lung and nasal epithelium carcinoma associated	12	97800_at	AI845714	NM_011126	NP_035256	2 H1	A	88.24%	palate, lung, and nasal epithelium expressed transcript Curated Ortholog	1.2	P	1	P	1	P	J. Biol. Chem. 274:13698-13703 (1999)
17	others	55442_g_at	palate, lung and nasal epithelium carcinoma associated	12	97800_at	AI845714	NM_011126	NP_035256	2 H1	A	88.24%	palate, lung, and nasal epithelium expressed transcript Curated Ortholog	1.2	P	1	P	1	P	J. Biol. Chem. 274:13698-13703 (1999)
17	others	63813_at	CGI-81 protein	13	169813_at	AV297782	NM_021554	NP_067529	7 F1-F2	C	98.06%	RIKEN cDNA 0610012D09 gene Curated Ortholog	0.71	A	1.7	A	0.77	A	Genome Res. 10:1617-1630 (2000)
17	others	63813_at	CGI-81 protein	14	95045_at	AI844469	NM_021554	NP_067529	7 F1-F2	A	98.06%	RIKEN cDNA 0610012D09 gene Curated Ortholog	1	P	1.3	P	0.91	P	Genome Res. 10:1617-1630 (2000)

cat #	category	human Probe ID	human title	#	mouse Probe ID	mouse GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	mouse chip ID	mouse homology	mouse name	MASM5 1st	MASM5 1st P/A	MASM5 2nd	MASM5 2nd P/A	MASM5 3rd	MASM5 3rd P/A	reference
25	structural protein	62998_at	keratin 6B		-	AF312019	-	-	-	-	89.50%	keratin complex 2, basic, pseudogene 1 (Krt2-ps1)	-		-		-		-

cat #	category	human Probe ID	human title	#	mouse Probe ID	mouse GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	mouse chip ID	mouse homology	mouse name	MASM5 1st	MASM5 1st P/A	MASM5 2nd	MASM5 2nd P/A	MASM5 3rd	MASM5 3rd P/A	reference
26	transcription factor	64071_at	papillomavirus regulatory factor PRF-1		none														
26	transcription factor	64121_at	glioma-amplified sequence-41	15	113151_at	AI854569	NM_026570	NP_080846	10 D2	B	89.84%	glioma-amplified sequence-41 Homolog	1	P	1.2	P	1	P	Meth. Enzymol. 303:19-44 (1999)
26	transcription factor	64121_at	glioma-amplified sequence-41	16	111096_i_at	AV045457	NM_026570	NP_080846	10 D2	C	89.84%	glioma-amplified sequence-41 Homolog	2.8	A	1.4	A	0.59	A	Meth. Enzymol. 303:19-44 (1999)
26	transcription factor	64121_at	glioma-amplified sequence-41	17	169003_f_at	AV121958	NM_026570	NP_080846	10 D2	C	89.84%	glioma-amplified sequence-41 Homolog	1.1	P	1	P	1	P	Meth. Enzymol. 303:19-44 (1999)

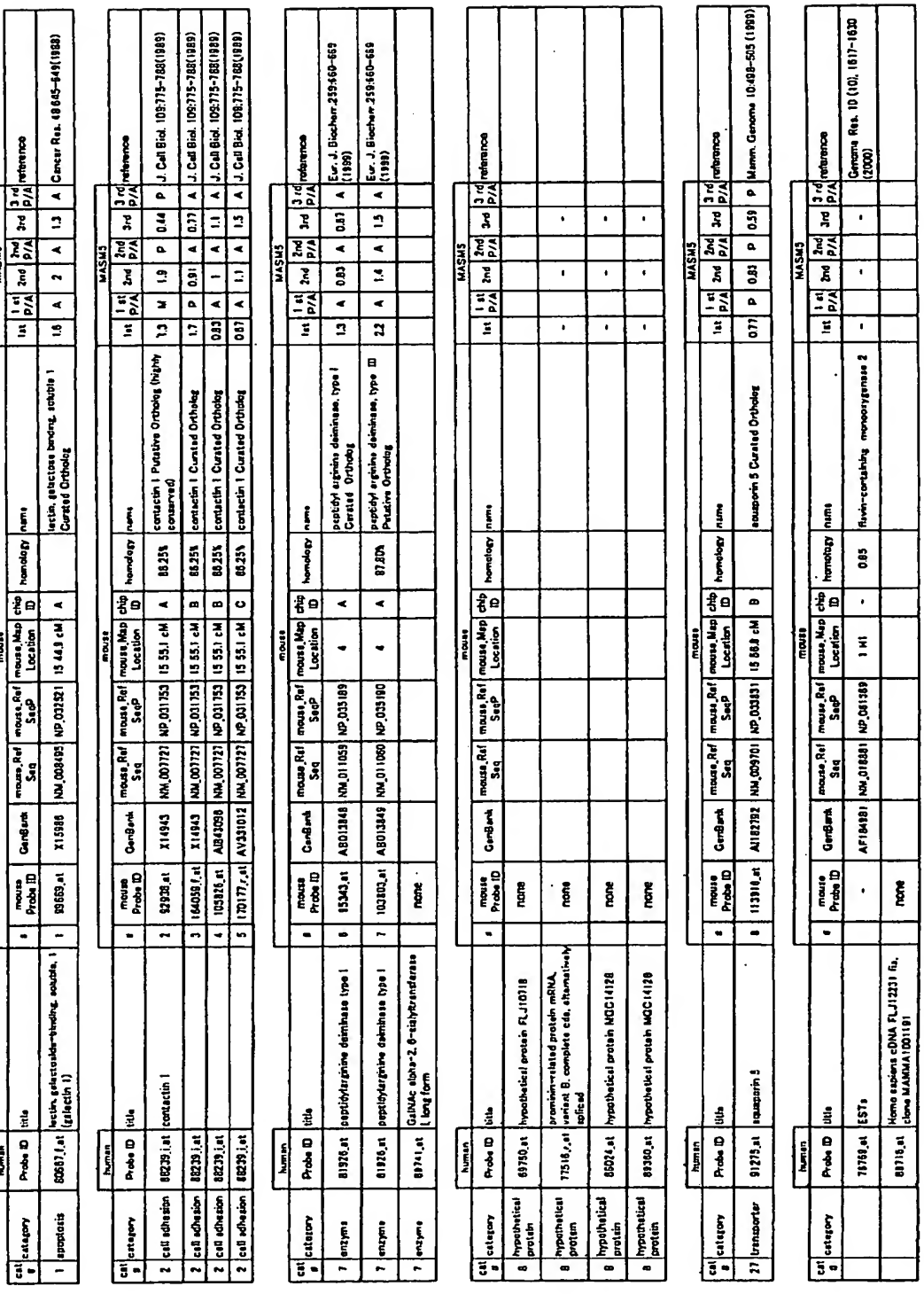
cat #	category	human Probe ID	human title	#	mouse Probe ID	mouse GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	mouse chip ID	mouse homology	mouse name	MASM5 1st	MASM5 1st P/A	MASM5 2nd	MASM5 2nd P/A	MASM5 3rd	MASM5 3rd P/A	reference
		64163_at	Homo sapiens clone 25194 mRNA sequence		none								-		-		-		
		65699_at	hypothetical protein		none								-		-		-		
		64285_at	ESTs		none														

Table 82



human				mouse								MASMS			
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
2	cell adhesion	79815_at	desmocollin 3 isoform a, b	1	97855_at	Y11169	NM_007882	NP_031908	18 7.0 cM	A	87.58%	desmocollin 3 Curated Ortholog	0.3	A	0.8	A	1.2	A	Dev. Dyn. 210:315-327 (1997)
human				mouse								MASMS							
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
5	cytokine related	74833_at	tumor necrosis factor, alpha-induced protein 2	2	160489_at	L24118	NM_009396	NP_033422	12 66.0 cM	A	83.78%	tumor necrosis factor, alpha-induced protein 2 Curated Ortholog	0.8	A	0.7	A	0.6	A	J. Biol. Chem. 269:3633-3640 (1994)
human				mouse								MASMS							
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
1	enzyme	74357_s_at	24-dehydrocholesterol reductase		none								-		-		-		
human				mouse								MASMS							
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
17	others	82721_at	ras homolog gene family, member V	3	131045_at	AU040173	-	-	-	C	90.77%	clone MGC:29291 IMAGE:5003149, Putative Ortholog	0.3	A	0.3	A	0.4	A	-
human				mouse								MASMS							
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
22	proteinase inhibitor	75248_at	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	4	101811_at	AB012693	NM_010581	NP_034711	16 B1	A	88.81%	integrin-associated protein Putative Ortholog	1	P	1	P	1	P	J. Cell Biol 123:485-496 (1993)
human				mouse								MASMS							
cat#	category	Probe ID	title	#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	mouse_Map Location	chip ID	homology	name	1st	1 st P/A	2nd	2nd P/A	3rd	3 rd P/A	reference
		69289_at	Homo sapiens cDNA FLJ12289 fis, clone MAMMA1001788	5	94780_at	AI981985	-	-	-	A	88.35%	DNA segment, Chr 18, Wayne State University 73, expressed Putative Ortholog	0.7	P	0.8	P	1	P	-
		69289_at		6	131442_at	AI893316	-	-	-	C	88.35%	DNA segment, Chr 18, Wayne State University 73, expressed Putative Ortholog	0.7	A	1	A	1.5	A	-
		70124_at	ESTs		none								-		-		-		
		72604_at	ESTs		none								-		-		-		
		73520_at	ESTs		none								-		-		-		
		83078_at	ESTs		none								-		-		-		
		83088_at	ESTs		none								-		-		-		
		84270_at	EST, Weakly similar to E48A_HUMAN E48 ANTIGEN PRECURSOR [H.sapiens]	7	120772_at	AI838844	NM_011838	NP_035968	15 D3	C	85.84%	Ly6/neurotoxin 1 Putative Ortholog	0.8	P	1.1	A	0.9	A	Neuron 22:- (1998)
		84270_at	EST, Weakly similar to E48A_HUMAN E48 ANTIGEN PRECURSOR [H.sapiens]	8	137205_f_at	AI838831	NM_011838	NP_035968	15 D3	C	85.84%	Ly6/neurotoxin 1 Putative Ortholog	0.2	A	0.4	A	0.7	A	Neuron 22:- (1998)
		84903_f_at	ESTs		none								-		-		-		
		87639_f_at	ESTs		none								-		-		-		
		88338_at	clone=IMAGE:2229660		none								-		-		-		

Table 83



[0229] In addition, the nucleotide sequences and the amino acid sequences of the mouse counterparts are shown

in SEQ ID NOs: 954 to 1635. The details are as follows.
The mouse counterparts of the human genes whose expression levels were increased by IL-13 (AI method):

954 to 1174 (nucleotide sequence)
1175 to 1375 (amino acid sequence)

The mouse counterparts of the human genes whose expression levels were decreased by IL-13 (IMM method):

1376 to 1505 (nucleotide sequence)
1506 to 1635 (amino acid sequence)

With respect to each mouse counterpart, Probe ID, GenBank Accession No., Ref SEQ NO, and the corresponding SEQ ID NO in the Sequence Listing are shown in Tables 84 to 113.

Table 84

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
2	160469_at	M62470	NM_011580	NP_035710	954	1376
2	92593_at	D13664	NM_015784	NP_056599	955	1377
2	101730_at	D82029	NM_007666	NP_031692	956	1378
2	101141_at	M33036	-	-	957	1379
2	95752_at	M90551	-	-	957	1379
2	none					
2	105606_at	AW210072	NM_028810	NP_083086	958	1380
2	163053_at	AA716925	NM_028810	NP_083086	958	1380

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
3	160545_at	M86183	NM_007632	NP_031658	959	1381
3	160545_at	M86183	NM_007632	NP_031658	959	1381

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
4	140659_at	AA174767	NM_019494	NP_062367	960	1382
4	93858_at	M33266	NM_021274	NP_067249	961	1383

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
5	95344_at	U65747	NM_008358	NP_032382	962	1384
5	93300_at	X57413	NM_009367	NP_033393	963	1385

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
6	97261_at	AF055664	NM_008295	NP_032324	964	1386
6	101979_at	AF055638	NM_011817	NP_035947	965	1387
6	109336_at	AI035425	NM_011817	NP_035947	965	1387

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
7	104420_at	U43428	NM_010927	NP_035057	966	1388
7	107939_at	AI021374	-	-	967	-
7	none					
7	114376_at	AW259579	NM_011961	NP_036091	968	1389
7	92834_at	U12620	NM_010074	NP_034204	969	1390
7	96918_at	AI790931	NM_019395	NP_062268	970	1391
7	165678_i_at	AI482191	-	-	971	-
7	-	X69657	NM_011710	NP_035840	972	1392
7	169670_at	AV028295	NM_008290	NP_032316	973	1393

Table 85

7	166141_i_at	AV224027	NM_008290	NP_032316	973	1393
7	101891_at	Y09517	NM_008290	NP_032316	973	1393
7	111949_at	AI853171	-	-	974	-
7	93085_at	D44458	NM_013585	NP_038613	975	1394
7	102717_at	X58077	-	-	976	1395
7	102717_at	X58077	-	-	976	1395
7	93352_at	M55154	NM_009373	NP_033399	977	1396
7	none					
7	161043_r_at	AV277568	NM_015762	NP_056577	978	1397
7	99985_at	AB027565	NM_015762	NP_056577	978	1397
7	161284_r_at	AV299386	NM_015762	NP_056577	978	1397
7	162642_at	AI854834	NM_015762	NP_056577	978	1397
7	-	AF159230	NM_019949	NP_064333	979	1398
7	94431_at	D16106	NM_009175	NP_033201	980	1399
7	167200_r_at	AV074481	NM_009175	NP_033201	980	1399
7	102410_at	AF019385	NM_010474	NP_034604	981	1400

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
8	110469_at	AI844322	-	-	982	-
8	109915_at	AA170781	NM_018851	NP_061339	983	1401
8	103080_at	U15635	NM_018851	NP_061339	983	1401
8	166390_at	AV245197	-	-	984	-
8	-	AK020957	-	-	985	-
8	-	BF321302	-	-	986	-
8	-	none	-	-		
8	-	none	-	-		

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
9	98822_at	X56602	NM_015783	NP_056598	987	1402
9	98822_at	X56602	NM_015783	NP_056598	987	1402
9	100981_at	U43084	NM_008331	NP_032357	988	1403
9	168299_f_at	AV090198	NM_008331	NP_032357	988	1403
9	100981_at	U43084	NM_008331	NP_032357	988	1403
9	168299_f_at	AV090198	NM_008331	NP_032357	988	1403
9	103432_at	AW122677	NM_020583	NP_065608	989	1404
9	105385_at	AI315194	NM_021384	NP_067359	990	1405
9	none					
9	98501_at	Y07519	NM_010743	NP_034873	991	1406
9	98500_at	D13695	NM_010743	NP_034873	991	1406
9	none					

Table 86

9	-	AW986054	-	-	992	-
9	-	AW986054	-	-	992	-
9	-	AK003407	-	BAB22771	993	1407
9	none					
9	none					
9	97444_at	AI844520	NM_023065	NP_075552	994	1408
9	164423_at	AV076807	NM_023065	NP_075552	994	1408
9	164273_at	AV276912	-	-	995	-

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
10	97823_g_at	AW122689	-	-	996	-
10	97822_at	AW122689	-	-	996	-
10	97821_at	AI646056	-	-	997	-
10	101435_at	AF033275	NM_009649	NP_033779	998	1409
10	163162_at	AI060985	NM_019921	NP_064305	999	1410
10	110116_at	AW124632	-	-	1000	-
10	100951_at	AF014010	NM_008861	NP_032887	1001	1411
10	99136_at	X63535	NM_009465	NP_033491	1002	1412

	mouse					
cat#	mouse Probe ID	GenBank	mouse Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
12	-	-	NM_008591	NP_032617	1003	1413
12	-	-	NM_008591	NP_032617	1003	1413
12	100309_at	Y00871	NM_008591	NP_032617	1003	1413
12	96935_at	AW011791	NM_026018	NP_080294	1004	1414
12	162531_at	AW048375	-	-	1005	-
12	101410_at	AB000713	NM_009903	NP_034033	1006	1415
12	100086_at	D00622	-	BAA00500	1007	-
12	161988_f_at	AV234541	-	-	1008	-
12	none					
12	104516_at	U82758	NM_013805	NP_038833	1009	1416
12	-	AY013776	NM_053140	NP_444370	1010	1417
12	103617_at	D63679	NM_010016	NP_034146	1011	1418
12	164905_r_at	AV358386	NM_010016	NP_034146	1011	1418
12	107626_at	AA174516	NM_010016	NP_034146	1011	1418
12	115133_at	AI875165	NM_021401, NM_026907	NP_067376, NP_081183	1012, 1013	1419, 1420

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO. (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
13	104509_at	AF059213	NM_009590	NP_034020	1014	1421
13	133666_at	AI450812	NM_009590	NP_034020	1014	1421

Table 87

13	98758_at	L34570	NM_009660	NP_033790	1015	1422
13	102696_s_at	AI747899	NM_019640	NP_062614	1016	1423
13	102696_e_at	AI747899	NM_019640	NP_062614	1016	1423
13	102697_at	U46934	NM_019640	NP_062614	1016	1423

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
14	101433_at	AF010452	NM_008209	NP_032235	1017	1424
14	none					
14	98438_f_at	X16202	NM_010394	NP_034524	1018	1425
14	98438_f_at	X16202	NM_010394	NP_034524	1018	1425

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
15	none					
15	101723_r_at	U06146	-	AAA18425	1019	1426
15	103024_at	X13335	NM_007403	NP_031429	1020	1427
15	92917_at	L36244	NM_010810	NP_034940	1021	1428
15	114151_at	AI426250	NM_010810	NP_034940	1021	1428
15	162318_r_at	AV069212	NM_010810	NP_034940	1021	1428

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
16	166806_at	AI835317	NM_019967	NP_064351	1022	1429

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
17	112883_at	AI835478	-	-	1023	-
17	100567_at	M20497	NM_024408	NP_077717	1024	1430
17	97912_at	AI843488	NM_019793	NP_062767	1025	1431
17	101429_at	X67083	NM_007837	NP_031863	1026	1432
17	97647_at	M11408	NM_013647	NP_038675	1027	1433
17	169860_r_at	M11408	NM_013647	NP_038675	1027	1433
17	169362_f_at	AV069368	NM_023137	NP_075626	1028	1434
17	92715_at	AV069368	NM_023137	NP_075626	1028	1434
17	168938_r_at	AV069368	NM_023137	NP_075626	1028	1434
17	112237_at	AI115916	NM_026228	NP_080504	1029	1435
17	97442_at	AI115916	NM_026228	NP_080504	1029	1435
27	110839_at	AI839647	-	-		

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
19	162702_at	AI851272	NM_019818	NP_062793	1030	1436

Table 88

19	165144_r_at	AV357104	NM_019819	NP_062793	1030	1436
19	171283_at	AV216631	NM_019819	NP_062793	1030	1436
19	182543_r_at	AV248162	NM_007388	NP_031414	1031	1437
19	98859_at	M99054	NM_007388	NP_031414	1031	1437

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (nucleotide seq.)
20	92832_at	U88315	NM_009896	NP_034026	1032	1438

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (nucleotide seq.)
21	101019_at	U74683	NM_009982	NP_034112	1033	1439
21	181251_f_at	AV316154	NM_009982	NP_034112	1033	1439
21	101020_at	AI842667	NM_009982	NP_034112	1033	1439
21	none					
21	-	AA798057	-	-	1034	-
21	93303_at	U64445	NM_011672	NP_035802	1035	1440

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (nucleotide seq.)
22	-	AF063937	NM_009126	NP_033152	1036	1441
22	108524_at	U64445	NM_011672	NP_035802	1037	1442
22	108524_at	U64445	NM_011672	NP_035802	1037	1442
22	96060_at	U25844	NM_009254	NP_033280	1038	1443
22	113899_at	AW121899	NM_007840	NP_031866	1039	1444
22	93493_at	X65627	NM_007840	NP_031866	1039	1444
22	137166_r_at	AI127311	NM_011111	NP_035241	1040	1445
22	92978_s_at	X16490	NM_011111	NP_035241	1040	1445

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (nucleotide seq.)
24	163453_at	AI596769	-	-	1041	-
24	166475_r_at	AV148353	-	-	1042	-
24	98307_at	AF106070	NM_011246	NP_035376	1043	1445
24	167498_i_at	AV313063	NM_011246	NP_035376	1043	1445
24	98417_at	M21038	NM_010846	NP_034976	1044	1447
24	103811_at	AB012693	NM_010581	NP_034711	1045	1448
24	102699_at	J03368	NM_013606	NP_038634	1046	1449
24	98417_at	M21038	NM_010846	NP_034976	1044	1447

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (nucleotide seq.)
25	-	AI427122	-	-	1047	-

Table 89

25	164428_i_at	AV085754	NM_008470	NP_032496	1048	1450
25	103589_at	AF053235	NM_008470	NP_032496	1048	1450

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
26	101465_at	U06924	NM_009283	NP_033309	1049	1451
26	114635_at	AA960121	NM_009283	NP_033309	1049	1451
26	101465_at	U06924	NM_009283	NP_033309	1049	1451
26	114635_at	AA960121	NM_009283	NP_033309	1049	1451
26	101465_at	U06924	NM_009283	NP_033309	1049	1451
26	101465_at	U06924	NM_009283	NP_033309	1049	1451
26	93281_at	AF049125	NM_011992	NP_036122	1050	1452
26	109154_at	AW121894	-	-	1051	-
26	-	AK005232	NM_027213	NP_081489	1052	1453
26	-	U73037	NM_016850	NP_058546	1053	1454
26	164758_i_at	AV222614	NM_017373	NP_059069	1054	1455

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
27	-	AF167411	NM_011867	NP_035997	1055	1456
27	102326_at	AB002664	NM_010877	NP_035007	1056	1457
27	110839_at	AI839647	-	-	1057	-

Table 90

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
2	none					
2	101730_at	D82029	NM_007666	P_031692	1058	1458

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
4	160596_at	AW050048	NM_025397	NP_079673	1059	1459
4	163760_at	AW122516	NM_023158	NP_075647	1060	1460
4	134771_at	AI606877	NM_023158	NP_075647	1060	1460
4	165377_r_at	AV062836	NM_023158	NP_075647	1060	1460

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
5	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
6	103471_at	AI194333	NM_025706	NP_079982	1061	1461
6	101955_at	AJ002387	NM_022310	NP_071705	1062	1462
6	162445_at	AV351546	NM_022310	NP_071705	1062	1462

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
7	167028_at	AI841650	NM_021890	NP_068690	1063	1463
7	168721_r_at	AV235789	NM_021890	NP_068690	1063	1463
7	104420_at	U43428	NM_010927	NP_035057	1064	1464
7	103446_at	AAA959954	NM_027835	NP_082111	1065	1465
7	99394_at	U86408	NM_008217	NP_032243	1066	1466
7	108048_at	AI836268	-	-	1067	-
7	none					
7	110639_at	AW108146	-	-	1068	-

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
8	107112_at	AI121797	-	-	1069	-
8	107112_at	AI121797	-	-	1069	-
8	116662_at	AI843057	-	-	1070	-
8	163364_at	AA472475	-	-	1071	-
8	168478_a_at	AV366153	-	-	1072	-
8	-	BE687722	-	-	1073	-
8	none					
8	-	AK020110	NM_029989	NP_084275	1074	1467
8	113253_r_at	AI852111	-	-	1075	-

Table 91

8	170461_i_at	AV209883	-	-	1078	-
8	115732_at	AI530075	-	-	1077	-
14	none					
8	106644_at	AW047110	NM_009370	NP_033396	1078	-
8	92427_at	D25540	NM_009370	NP_033396	1078	-
8	none					
8	none					
8	none					
8	106644_at	AW047110	NM_009370	NP_033396	1078	1468
8	92427_at	D25540	NM_009370	NP_033396	1078	1468
8	102907_at	AW125043	-	-	1079	-
8	106644_at	AW047110	NM_009370	NP_033396	1078	-
8	92427_at	D25540	NM_009370	NP_033396	1078	-
8	none					
8	114794_at	AA693185	-	-	1080	-
8	none					
8	92971_at	AW125849	-	-	1081	-
8	102907_at	AW125043	-	-	1079	-
8	114119_at	AW124823	-	-	1082	-
8	112671_at	AW122101	-	-	1083	-
8	112671_at	AW122101	-	-	1083	-
8	none					
8	none					
8	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
9	none					
9	95974_at	M55544	NM_010259	NP_034389	1084	1469

	mouse					
cat#	mouse Probe ID	GenBank	mouse Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
10	101435_at	AF033275	NM_009649	NP_033779	1085	1470
10	AA060013	-	-	-	1086	-
10	103839_at	AF06474B	NM_011451	NP_035581	1087	1471
10	164777_i_at	AV250525	NM_011451	NP_035581	1087	1471
10	162448_f_at	AV354094	NM_030704	NP_109629	1088	1472
10	160139_at	AI848798	NM_030704	NP_109629	1088	1472

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
12	160415_at	AI604314	NM_016674	NP_057883	1089	1473
12	97546_at	AF077127	NM_016674	NP_057883	1089	1473
12	99934_at	M80206	NM_008990	NP_033016	1090	1474
12	164850_f_at	AV359774	NM_008990	NP_033016	1090	1474

Table 92

12	99933_at	D26107	NM_008990	NP_033016	1090	1474
12	103811_at	AA991032	-	-	1091	-
12	170500_at	AV223427	-	-	1092	-

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
16	163337_at	AA727483	-	-	1093	-
16	109021_at	AW214142	NM_030253	NP_084529	1094	1475

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
17	109915_at	AA170781	NM_018851	NP_061339	1095	1476
17	103080_at	U15635	NM_018851	NP_061339	1095	1476
17	AW742692	-	-	-	1096	-
17	166458_at	AJ431004	NM_025872	NP_080148	1097	1477
17	107906_at	AI316570	NM_025872	NP_080148	1097	1477
17	165304_at	AV245062	NM_138741	NP_620080	1098	1478
17	160373_i_at	AI839175	NM_138741	NP_620080	1098	1478
17	111260_at	AI843809	-	-	1099	-
17	166340_at	AA793551	-	-	1100	-
17	165319_at	AV270997	NM_016736	NP_058016	1101	1479
17	168781_at	AV258801	NM_020622	NP_065647	1102	1480
17	161580_f_at	AV314829	NM_016736	NP_058016	1101	1479
17	100570_at	U27462	NM_016736	NP_058016	1101	1479
17	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
18	104550_at	AW123273	NM_028775	NP_083051	1103	1481

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
20	92832_at	U88325	NM_009896	NP_034026	1104	1482
20	93281_at	AF049125	NM_011992	NP_036122	1105	1483

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO (amino acid seq.)
21	93024_at	AW047653	NM_011909	NP_036039	1106	1484

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
24	162383_r_at	AV248832	NM_009895	NP_034025	1107	1485
24	100022_at	D89613	NM_009895	NP_034025	1107	1485
24	115398_at	AW212285	NM_020578	NP_065603	1108	1486

Table 93

24	163326_i_at	AI616268	NM_021178	NP_081454	1109	1487

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
25	163157_at	AI606261	NM_033373	NP_203537	1110	1488

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
26	-	-	NM_016850	NP_058546	1111	1489
26	161185_i_at	AV235936	NM_010637	NP_034767	1112	1490
26	99622_at	U20344	NM_010637	NP_034767	1117	1490

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP		
	none					
	none					
	none					
	161081_at	AA733664	-	-	1113	-
	none					
	none					
	none					
	none					
	none					
	95020_at	AI848858	-	-	1114	-
	none					

Table 94

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
3	101469_at	AF009365	NM_017464	NP_059497	1115	1491

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
5	162349_i_at	AV173028	NM_019959	NP_064343	1116	1492
5	162365_i_at	AV231477	NM_019959	NP_064343	1116	1492
5	161549_f_at	AV246051	NM_019959	NP_064343	1116	1492
5	103576_at	AI551306	NM_019959	NP_064343	1116	1492
5	162487_f_at	AV122373	NM_019959	NP_064343	1116	1492

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
7	-	AF338440	NM_053083	NP_444313	1117	1493

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
8	none					
8	114164_at	AW214638	-	-	1118	-
8	none					
8	110625_at	AI591648	-	-	1119	-
8	105356_at	AI007408	-	-	1120	-
8	112743_at	AI157595	-	-	1121	-
8	112061_at	AI465433	-	-	1122	-
8	133797_at	AI116550	NM_139065	NP_620704	1123	1494
8	112295_at	AA759831	NM_139065	NP_620704	1123	1494
8	111841_at	AI527658	-	-	1124	-
8	133349_at	AI037551	-	-	1125	-
8	102965_at	AW121646	-	-	1126	-
8	112671_at	AW122101	-	-	1127	-

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
9	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
12	92626_at	X67209	NM_008721	NP_032747	1128	1495
12	96935_at	AW011791	NM_026018	NP_080294	1129	1496
12	162531_at	AW048375	-	-	1130	-
12	96935_at	AW011791	NM_026018	NP_080294	1129	1496
12	162531_at	AW048375	-	-	1130	-

Table 95

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
14	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
16	107575_at	AA980835	-	-	1131	-

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
17	169317_at	AV044941	NM_022028	NP_071311	1132	1497
17	111119_at	AA764217	NM_022028	NP_071311	1132	1497
17	111162_f_at	AA014158	NM_022028	NP_071311	1132	1497
17	114337_at	AW122502	NM_022028	NP_071311	1132	1497
17	112893_at	AI842196	NM_022028	NP_071311	1132	1497
17	169317_at	AV044941	NM_022028	NP_071311	1132	1497
17	111119_at	AA764217	NM_022028	NP_071311	1132	1497
17	111162_f_at	AA014158	NM_022028	NP_071311	1132	1497
17	114337_at	AW122502	NM_022028	NP_071311	1132	1497
17	112893_at	AI842196	NM_022028	NP_071311	1132	1497
17	115316_at	AI550677	-	-	1133	-
17	168371_f_at	AV254276	-	-	1134	-
17	106282_at	AA914186	-	-	1135	-
17	188490_at	AI562368	-	-	1136	-
17	none					
17	114263_at	AW121271	-	-	1137	-

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
21	109965_s_at	AA938946	NM_015775	NP_056590	1138	1498
21	131180_at	AI607826	NM_015775	NP_056590	1138	1498
21	164520_f_at	AV302474	NM_015775	NP_056590	1138	1498
21	101019_at	U74683	NM_009982	NP_034112	1139	1499
21	161251_f_at	AV316954	NM_009982	NP_034112	1139	1499
21	101020_at	AI842687	NM_009982	NP_034112	1139	1499

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
24	-	AF233517	NM_021893	NP_068693	1140	1500

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
25	163157_at	AI806261	NM_033373	NP_203537	1141	1501
25	129268_at	AW122522	-	-	1142	-

Table 96

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
	103066_at	L32973	NM_020557	NP_065582	1143	1502
	161186_f_at	AV246064	NM_020557	NP_065582	1143	1502
	none					
	none					
	none					
	none					
	none					

Table 97

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
7	102741_at	AW046250	NM_019655	NP_062629	1144	1503
7	96188_at	AF052506	NM_019655	NP_062629	1144	1503
7	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
8	none					
8	none					
8	none					
8	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
9	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
24	102699_at	J03358	NM_013606	NP_038634	1145	1504
24	98417_at	M21038	NM_010846	NP_034976	1146	1505

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
	none					
	none					
	none					
	none					
	none					

Table 98

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
2	134563_at	AI592213	-	-	1147	-
2	110160_at	AI510217	-	-	1148	-

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
4	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
7	-	U42443	NM_007532	NP_031558	1149	1506
7	-	U42443	NM_007533	NP_031558	1150	1506
7	none					
7	132809_at	AA762195	-	-	1151	-
7	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
8	92909_at	X80171	NM_008827	NP_032853	1152	1507
8	none					
8	102907_at	AW125043	-	-	1153	-
8	none					
8	110028_at	AW124261	-	-	1154	-
8	112808_at	AI853680	-	-	1155	-
8	116098_at	AI546866	-	-	1156	-
8	107796_at	AW261774	-	-	1157	-
8	none					
8	161378_f_at	AV243059	NM_133349	NP_579927	1158	1508
8	160713_at	AI841579	NM_133349	NP_579927	1158	1508
8	167609_r_at	AW121990	-	-	1159	-
8	94733_at	AW048842	NM_054099	NP_473440	1160	1509

	mouse					
cat#	mouse Probe ID	GenBank	mouse Ref Seq	mouse Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
9	103385_at	AI315194	NM_021384	NP_067359	1161	1510

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
12	160415_at	AI604314	NM_016674	NP_057883	1162	1511
12	97546_at	AF072127	NM_016674	NP_057883	1162	1511
12	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
16	109021_at	AW214142	NM_030253	NP_084529	1163	1512
16	163337_at	AA727483	-	-	1164	-

Table 99

16	163337_at	AA727483	-	-	1164	-

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
17	162006_r_at	AV334115	-	-	1165	-
17	100589_at	AW047808	-	-	1166	-
17	133126_at	AW107849	-	-	1167	-
17	102243_at	AF035527	NM_007914	NP_031940	1168	1513
17	114753_at	AW215423	NM_007914	NP_031940	1168	1513
17	110963_at	AI527695	NM_007914	NP_031940	1168	1513
17	114753_at	AF035527	NM_007914	NP_031940	1168	1513
17	102243_at	AW215423	NM_007914	NP_031940	1168	1513
17	110963_at	AI527695	NM_007914	NP 031940	1168	1513
17	108958_at	AI851818	-	-	1169	-
17	93342_at	AI852665	-	-	1170	-
17	92389_at	AB025411	NM_011856	NP_035985	1171	1514
17	133154_at	AW125558	-	-	1172	-

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
20	135407_at	AW226597	-	-	1173	-

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
24	-	AF268195	NM_030732	NP_109657	1174	1515

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
27	none					
27	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
	none					

Table 100

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
1	99669_at	X15986	NM_008495	NP_032521	1175	1516

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
2	none					
2	161239_r_at	AV281306	NM_007697	NP_031723	1176	1517
2	103088_at	X94310	NM_007697	NP_031723	1176	1517
2	167319_i_at	AV283855	NM_007697	NP_031723	1176	1517
2	169984_i_at	AV278112	NM_007697	NP_031723	1176	1517
2	-	A46528	-	-	1177	-
2	100019_at	D45889	NM_019389	NP_062262	1178	1518
2	161370_f_at	AV239731	NM_011519	NP_035649	1179	1519
2	96033_at	Z22532	NM_011519	NP_035649	1179	1519
2	165372_at	AV056802	-	-	1180	-

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
4	164885_f_at	AV335220	NM_009142	NP_033168	1181	1520
4	98008_at	U92565	NM_009142	NP_033168	1181	1520
4	161752_r_at	AV280053	NM_009142	NP_033168	1181	1520

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
5	161157_r_at	AV231282	NM_009369	NP_033395	1182	1521
5	92877_at	L19932	NM_009369	NP_033395	1182	1521
5	160489_at	L24118	NM_009369	NP_033395	1182	1521

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
6	161593_r_at	AV291690	-	-	1183	-
6	103242_at	AW123834	NM_009677	NP_033807	1184	1522
6	92288_at	X54424	NM_009677	NP_033807	1184	1522
6	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
7	none					
7	94908_at	M22679	NM_007409	NP_031435	1185	1523
7	106011_at	AW261476	NM_018881	NP_061369	1186	1524
7	165790_at	AA681923	NM_018984	NP_064368	1187	1525
7	94908_at	M22679	NM_007409	NP_031435	1185	1523

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7	103905_at	AI314958	-	-	1188	-
7	none					
7	164478_r_at	AV248818	NM_033198	NP_573461	1189	1526
7	110291_at	AI256150	NM_033198	NP_573461	1189	1526
7	none					
7	162221_i_at	AV112892	-	-	1190	-
7	94842_at	AI853830	-	-	1191	-
7	162179_r_at	AV367274	-	-	1192	-
7	none					
7	160937_at	AF039391	NM_016669	NP_057878	1193	1527
7	166000_at	AV248813	NM_016669	NP_057878	1193	1527
7	101587_at	U89419	NM_010145	NP_034275	1194	1528
7	92851_at	U49430	NM_007752	NP_031778	1195	1529
7	93688_at	D21826	NM_007717	NP_031743	1196	1530
7	94507_at	U15977	NM_007981	NP_032007	1197	1531
7	117284_at	AI848384	NM_008131	NP_032157	1198	1532
7	99498_at	M60803	NM_008131	NP_032157	1198	1532
7	94852_at	U09114	NM_008131	NP_032157	1198	1532
7	161826_r_at	AV381947	NM_008131	NP_032157	1198	1532
7	101991_at	D16215	NM_010231	NP_034361	1199	1533
7	104421_at	U87147	NM_008030	NP_032056	1200	1534
7	158706_r_at	AV225591	NM_008161	NP_032187	1201	1535
7	101678_at	U13705	NM_008161	NP_032187	1201	1535

			mouse			
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
8	113969_at	AW208826	-	-	1202	-
8	none					
8	135485_r_at	AV242700	-	-	1203	-
8	162919_at	AI227478	-	-	1204	-
8	112372_at	AW230421	-	-	1205	-
8	108490_at	AI463227	-	-	1206	-
8	94418_at	AI839004	NM_130450	NP_569717	1207	1536

			mouse			
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
10	169261_at	AV298003	NM_023580	NP_076069	1208	1537
10	100143_at	Y07711	NM_011727	NP_035907	1209	1538
10	103451_at	AI835159	-	-	1210	-
10	169902_at	AV214820	-	-	1211	-
10	167168_i_at	AV127592	-	-	1212	-
10	160067_at	AW125329	-	-	1213	-

Table 102

10	93422_at	U62391	NM_011074	NP_035204	1214	1539
10	93421_at	AF033855	NM_011074	NP_035204	1214	1539
10	168913_r_at	AV347594	NM_011074	NP_035204	1214	1539
10	167725_f_at	AI847882	NM_011074	NP_035204	1214	1539
10	113157_at	AI850672	NM_016856	NP_058562	1215	1540
10	160806_at	AF099988	NM_016856	NP_058562	1215	1540

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
11	96947_at	AW048273	-	-	1216	-
11	162144_at	AV351508	-	-	1217	-
11	107600_at	AI838753	-	-	1218	-
11	98054_at	L33418	NM_007899	NP_031925	1219	1541
11	170917_r_at	AV092620	NM_007899	NP_031925	1219	1541
11	160841_at	AI021573	NM_133232	NP_573495	1220	1542
11	103577_at	AI326331	NM_133232	NP_573495	1220	1542

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
12	118451_at	AA615200	-	-	1221	-
12	118451_at	AA615200	-	-	1221	-
12	none					
12	160509_at	AW208486	-	-	1222	-
12	-	AH009304	NM_017369	NP_059065	1223	1543
12	93430_at	AF000236	NM_007722	NP_031748	1224	1544
12	99915_at	L41352	NM_009704	NP_033834	1225	1545
12	96339_at	AW048363	NM_053257	NP_444487	1226	1546
12	167252_at	AV106158	NM_053257	NP_444487	1226	1546
12	164621_i_at	AV157335	NM_053257	NP_444487	1226	1546
12	108822_at	AI515758	NM_053110	NP_444340	1227	1547
12	108824_at	AV223501	NM_053110	NP_444340	1227	1547
12	92956_at	X74760	NM_008716	NP_032742	1228	1548
12	98387_at	L26047	NM_009747	NP_033877	1229	1549
12	129282_at	AW124518	NM_019571	NP_062517	1230	1550
12	140325_at	AW125637	NM_019571	NP_062517	1230	1550
12	163391_at	AW123971	NM_019571	NP_062517	1230	1550
12	82426_at	AI877157	NM_019571	NP_062517	1230	1550

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
13	92494_at	AJ238978	NM_011922	NP_035052	1231	1551

Table 103

13	-	AJ011800	NM_010030	NP_034160	1232	1552
13	98420_at	AA919924	NM_053261	NP_444449	1233	1553
13	AI505678	-	-	-	1234	-
13	161918_at	AV380611	NM_009731	NP_033861	1235	1554
13	102826_at	J05663	NM_009731	NP_033861	1235	1554
13	132885_at	AI429094	-	-	1236	-
13	160544_at	AJ223066	NM_010634	NP_034764	1237	1555
13	109764_at	AI840194	NM_010634	NP_034764	1237	1555

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
14	100998_at	M21932	NM_010379	NP_034509	1238	1556
14	116266_at	AW122580	NM_010382	NP_034512	1239	1557
14	100998_at	M21932	NM_010379	NP_034509	1238	1556
14	116266_at	AW122580	NM_010382	NP_034512	1239	1557

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
15	94724_at	Y13185	NM_019471	NP_062344	1240	1558
15	162369_f_at	AV238570	NM_013599	NP_038627	1241	1559
15	89957_at	X72785	NM_013599	NP_038627	1241	1559
15	168521_r_at	AV231860	NM_013599	NP_038627	1241	1559

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
16	161718_at	AV252298	NM_010234	NP_034364	1242	1560
16	160901_at	V00727	NM_010234	NP_034364	1242	1560
16	167990_at	AA118615	-	-	1243	-
16	161716_at	AV252298	NM_010234	NP_034364	1242	1560
16	160901_at	V00727	NM_010234	NP_034364	1242	1560
16	167990_at	AA118615	-	-	1243	-
16	93508_at	AW121063	NM_133868	NP_598629	1244	1561
16	160458_s_at	U60553	NM_1010884	NP_035014	1245	1562
16	110774_at	AI852667	-	-	1246	-
16	183286_at	AW122051	-	-	1247	-
16	101078_r_at	AB016592	NM_011783	NP_035913	1248	1563
16	101075_f_at	AB016592	NM_011783	NP_035913	1248	1563
16	162200_r_at	AV062476	NM_011783	NP_035913	1248	1563

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
17	106586_at	AI152881	-	-	1248	-

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17	171229_r_at	AV167732	-	-	1250	-
17	none					
17	none					
17	162559_at	AI837711	-	-	1251	-
17	168765_at	AV245837	-	-	1252	-
17	111732_at	AA881910	-	-	1253	-
17	108756_at	AW045893	NM_134094	NP_598855	1254	1564
17	112376_at	AW124163	NM_134094	NP_598855	1254	1564
17	140699_at	AW124014	-	-	1255	-
17	103460_at	AI849939	-	-	1256	-
17	163822_at	AA073823	NM_133743	NP_598504	1257	1565
17	169732_i_at	AV075775	NM_133743	NP_598504	1257	1565

	mouse					
cat#	mouse Probe ID	GenBank	mouse Ref Seq	mouse Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
18	102701_at	M21856	-	AAA40425	1258	1566
18	102890_at	AF047529	NM_007814	NP_031840	1259	1567
18	none					
18	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
19	168611_i_at	AV216941	NM_013642	NP_038670	1260	1568
19	104598_at	X61940	NM_013642	NP_038670	1260	1568
19	92380_r_at	AJ133130	NM_011219	NP_035349	1261	1569
19	169828_f_at	AV151279	NM_011219	NP_035349	1261	1569
19	134749_f_at	AI662731	NM_011219	NP_035349	1261	1569
19	165782_at	AW120652	-	-	1262	-

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
20	95083_at	X81581	NM_008343	NP_032369	1263	1570
20	95082_at	AI842277	NM_008343	NP_032369	1263	1570
20	95083_at	X81581	NM_008343	NP_032369	1263	1570
20	95082_at	AI842277	NM_008343	NP_032369	1263	1570
20	103904_at	X81584	NM_008344	NP_032370	1264	1571
20	100715_at	U89840	NM_020597	NP_065622	1265	1572

	mouse					
cat#	mouse Probe ID	GenBank	mouse Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
21	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
22	-	AK018226	XM_110043	XP_110043	1266	1573

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22	103611_at	AB012693	NM_010581	NP_034711	1267	1574
22	94147_at	M33960	NM_008871	NP_032897	1268	1575
22	94147_at	M33960	NM_008871	NP_032897	1268	1575
22	170241_f_at	AV077498	NM_009257	NP_033283	1269	1576
22	100034_at	U54705	NM_009257	NP_033283	1269	1576
22	165730_at	AI648751	NM_009257	NP_033283	1269	1576

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
23	101634_at	M33212	NM_008722	NP_032748	1270	1577
23	103448_at	M83218	NM_013650	NP_038678	1271	1578
23	188722_r_at	AV360070	NM_008722	NP_032748	1272	1577
23	165723_at	AV295738	NM_008722	NP_032748	1272	1577

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
24	137179_at	AI325535	-	-	1273	-
24	100127_at	M35523	-	AAA37454	1274	1579
24	137179_at	AI325535	-	-	1273	-
24	100127_at	M35523	-	AAA37454	1274	1579
24	110236_at	AI430293	-	-	1275	-
24	110236_at	AI430293	-	-	1275	-
24	165779_i_at	AW124292	-	-	1276	-
24	94291_at	L04503	NM_011681	NP_035811	1277	1580
24	109308_at	AI503500	-	-	1278	-
24	94712_at	U73620	NM_009506	NP_033532	1279	1581
24	103579_at	X53247	NM_009008	NP_033034	1280	1582

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
25	101046_at	X56397	NM_011701	NP_035831	1281	1583
25	162379_r_at	AV245272	NM_011701	NP_035831	1281	1583
25	161361_s_at	AV213431	NM_011618	NP_035748	1282	1584
25	101383_at	AJ131711	NM_011618	NP_035748	1282	1584
25	92739_at	L28819	NM_008412	NP_032438	1283	1585
25	113796_at	AI314966	NM_024427	NP_077745	1284	1586
25	105003_at	AA939674	NM_024427	NP_077745	1284	1586
25	160532_at	M22479	NM_024427	NP_077745	1284	1586
25	113796_at	AI314966	NM_024427	NP_077745	1284	1586
25	105003_at	AA939674	NM_024427	NP_077745	1284	1586
25	160532_at	M22479	NM_024427	NP_077745	1284	1586

Table 106

25	113796_at	AI314966	NM_024427	NP_077745	1284	1586
25	105003_at	AA939674	NM_024427	NP_077745	1284	1586
25	160527_at	M22479	NM_024427	NP_077745	1284	1586
25	100446_r_at	X91825	NM_009265	NP_033291	1285	1587
25	100445_f_at	X91825	NM_009265	NP_033291	1285	1587
25	164632_i_at	AV225959	-	-	1286	-
25	160852_at	D16313	NM_008469	NP_032495	1287	1588
25	164618_f_at	AV171812	NM_008469	NP_032495	1287	1588
25	163295_at	AI561819	NM_025276	NP_079552	1288	1589

	mouse					
cat#	mouse Probe ID	GenBank	mouse Ref Seq	mouse Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
26	98122_at	AF074600	NM_010723	NP_034853	1289	1590
26	99052_at	D76432	NM_011546	NP_035676	1290	1591
26	104645_at	AI853712	NM_033563	NP_291041	1291	1592
26	112898_at	AW045576	NM_033563	NP_291041	1291	1592
26	107020_at	AW049268	NM_033563	NP_291041	1291	1592
26	114906_at	AI646497	NM_033563	NP_291041	1291	1592
26	100736_at	L77900	NM_013800	NP_038828	1292	1593
26	100050_at	M31885	-	AAA37879	1293	1594
26	97487_at	X70298	NM_009255	NP_033281	1294	1595

	mouse					
cat#	mouse Probe ID	GenBank	mouse Ref Seq	mouse Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
27	103800_at	AB019003	NM_013790	NP_038818	1295	1596
27	165744_at	AW124768	NM_013790	NP_038818	1295	1596
27	169447_r_at	AV168159	NM_013790	NP_038818	1295	1596
27	100064_f_at	M63801	NM_010288	NP_034418	1296	1597
27	100063_r_at	M63801	NM_010288	NP_034418	1296	1597
27	113916_at	AI182792	NM_009701	NP_033831	1297	1598
27	92792_at	U69135	NM_011871	NP_035801	1298	1599
27	110692_at	AJ606832	NM_011325	NP_035455	1299	1600
27	-	AK010437	NM_027399	NP_081675	1300	1601
27	163918_at	AV216203	-	-	1301	-
27	169112_r_at	AV216203	-	-	1301	-

	mouse					
cat#	mouse Probe ID	GenBank	mouse Ref Seq	mouse Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
	none					
	140497_at	AW124202	-	-	1302	-
	131152_at	AW142707	-	-	1303	-

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	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
2	97655_at	Y11169	NM_007882	NP_031908	1304	1602
2	97655_at	Y11169	NM_007882	NP_031908	1304	1602

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
5	-	BB850070	-	-	1305	-

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
7	106071_at	AI852199	-	-	1306	-
7	109537_at	AW122537	NM_019835	NP_062809	1307	1603
7	93015_at	X65021	NM_010056	NP_034486	1308	1604
7	164617_i_at	AV168894	NM_010056	NP_034486	1308	1604
7	103865_at	AW12253	NM_130450	NP_569717	1309	1605
7	94418_at	AI839004	NM_130450	NP_569717	1309	1605

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
8	102258_at	AF062476	NM_009294	NP_033317	1310	1606
8	103460_at	AI849939	NM_029083	NP_083359	1311	1607
8	none					
8	167736_r_at	AV212218	NM_133687	NP_598448	1312	1608
8	95701_at	AW124069	NM_133687	NP_598448	1312	1608
8	110541_at	AI843915	-	-	1313	-
8	106088_at	AI844788	-	-	1314	-
8	165731_at	AV204596	-	-	1315	-
8	162562_at	AI840292	NM_023270	NP_075759	1316	1609
8	108010_at	AW210455	NM_023270	NP_075759	1318	1609
8	none					
8	-	AW048177	-	-	1317	-
8	none					
8	none					
8	162963_at	AI835402	-	-	1318	-
8	none					
8	none					
8	115700_at	AI314284	NM_025807	NP_080083	1319	1610
8	-	AK003761	NM_028861	NP_083117	1320	1611
8	none					
8	104880_at	AW121537	-	-	1321	-
8	102018_at	AI854879	-	-	1322	-
8	none					
8	115700_at	AI314284	NM_025807	NP_080083	1319	1610

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8	115700_at	AI314284	NM_025807	NP_080083	1319	1610
8	-	X73360	-	CAA51770	1323	1612
8	none					

	mouse					
cat8	mouse Probe ID	GenBank	mouse Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
10	96570_at	AV381276	-	-	1324	-
10	111191_at	AW120521	-	-	1325	-

	mouse					
cat8	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
11	none					

	mouse					
cat8	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
12	101913_at	AW214298	NM_010423	NP_034553	1326	1613
12	170560_r_at	AV333303	NM_010423	NP_034553	1326	1613
12	161451_r_at	AV292193	NM_010423	NP_034553	1326	1613
12	95671_at	AJ243895	NM_010423	NP_034553	1326	1613

	mouse					
cat8	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
16	none					

	mouse					
cat8	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
17	none					
17	none					
17	94370_at	AA615075	-	-	1327	-
17	94370_at	AA615075	-	-	1327	-
17	160446_at	U46068	-	AAA87581	1328	1614
17	171144_i_at	AV087463	-	-	1329	-
17	168955_i_at	AV092579	-	-	1330	-
17	169746_at	AV090198	-	-	1331	-
17	-	AI845714	NM_011126	NP_035255	1332	1615

	mouse					
cat8	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
20	94297_at	U18939	NM_010220	NP_034350	1333	1616
20	100636_at	U28656	NM_007918	NP_031944	1334	1617

	mouse					
cat8	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
25	92313_at	AI844085	NM_007730	NP_031756	1335	1618
25	92314_at	U25652	NM_007730	NP_031756	1335	1618

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	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
27	109069_at	AI255982	NM_016917	NP_058613	1336	1619
27	97759_at	U09383	NM_010810	NP_034740	1337	1620
27	97759_at	U09383	NM_010810	NP_034740	1337	1620
27	98994_at	AF081499	NM_011402	NP_035532	1338	1621
27	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
	none					
	none					
	94637_at	X85992	-	CAA59984	1339	1622
	none					
	none					
	none					
	114451_at	AI848332	-	-	1340	-
	93178_at	AW050346	-	-	1341	-
	none					
	none					
	96220_at	AW123157	-	-	1342	-
	160978_at	AW261569	-	-	1343	-
	none					
	108954_at	AW060536	NM_025980	NP_080256	1344	1623
	164706_at	AV022728	NM_025980	NP_080256	1344	1623
	none					
	170083_r_at	AV338868	-	-	1345	-
	117306_at	AW120879	-	-	1346	-
	170414_i_at	AV333624	-	-	1347	-
	105944_at	AI844171	-	-	1348	-
	none					

Table 110

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
3	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
4	96953_at	AW120786	NM_019568	NP_062514	1349	1624

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
8	113969_at	AW208826	-	-	1350	-
8	-	BB553960	-	-	1351	-
8	163461_at	AA589180	NM_024246	NP_077208	1352	1625
8	170263_f_at	AV092570	NM_024246	NP_077208	1352	1625
8	none					
8	none					
8	none					
8	163845_i_at	AA387607	NM_026345	NP_080621	1353	1626
8	111405_at	AI847396	-	-	1354	-
8	111405_at	AI847396	-	-	1354	-
8	none					
8	98092_at	AA790307	NM_139198	NP_631937	1355	1627
8	none					
8	103858_at	AI847445	-	-	1356	-
8	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
10	97525_at	U48403	NM_008194	NP_032220	1357	1628
10	169383_r_at	AV087577	NM_008194	NP_032220	1357	1628

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
12	160508_at	AW209486	-	-	1358	-

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
17	97900_at	AI845714	NM_011126	NP_035256	1359	1629
17	97900_at	AI845714	NM_011126	NP_035256	1359	1629
17	169613_at	AV297752	NM_021554	NP_067529	1360	1630
17	95045_at	AI844469	NM_021554	NP_067529	1360	1630

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
25	-	AF312019	-	-	1361	-

Table 111

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
26	none					
26	113151_at	AI854569	NM_026570	NP_080846	1362	1631
26	171096_i_at	AV045457	NM_026570	NP_080846	1362	1631
26	169003_f_at	AV121958	NM_026570	NP_080846	1362	1631

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
	none					
	none					
	none					

Table 112

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
2	97655_at	Y11169	NM_007882	NP_031908	1363	1632

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP		
5	160489_at	L24118	NM_009396	NP_033422	1364	1633

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP		
7	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP		
17	133045_at	AU040173	-	-	1365	-

	mouse					
cat#	mouse Probe ID	GenBank	mouse Ref Seq	mouse Ref SeqP		
22	103611_at	AB012693	NM_010581	NP_034711	1366	1634

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP		
	94780_at	AI987985	-	-	1367	-
	136442_at	AI593316	-	-	1368	-
	none					
	none					
	none					
	none					
	none					
	130772_at	AI838844	NM_011838	NP_035968	1369	1635
	137205_f_at	AI839851	NM_011838	NP_035968	1369	1635
	none					
	none					
	none					

Table 113

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
1	99669_at	X15986	NM_008495	NP_032521	1370	1636

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
2	92936_at	X14943	NM_007727	NP_031753	1371	1637
2	164059_f_at	X14943	NM_007727	NP_031753	1371	1637
2	105826_at	AI843096	NM_007727	NP_031753	1371	1637
2	170177_r_at	AV331012	NM_007727	NP_031753	1371	1637

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
7	95343_at	AB013848	NM_011059	NP_035189	1372	1638
7	103803_at	AB013849	NM_011060	NP_035190	1373	1639
7	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
8	none					
8	none					
8	none					
8	none					

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
27	113916_at	AI182792	NM_009701	NP_033831	1374	1640

	mouse					
cat#	mouse Probe ID	GenBank	mouse_Ref Seq	mouse_Ref SeqP	SEQ ID NO: (nucleotide seq.)	SEQ ID NO: (amino acid seq.)
	-	AF184981	NM_018881	NP_061369	1375	1641
	none					

5. Determination of the expression levels of the genes narrowed down in Section 4 in the human goblet cell differentiation model and the mouse OVA antigen-exposed bronchial hypersensitivity model

[0230] Eighty-eight genes, most of which were recognized as genes whose expression levels were altered in human and mouse, were selected from the genes narrowed down in Section 4. A quantitative PCR assay was carried out with ABI 7700 using cDNA from the human goblet cell differentiation model and using cDNA from the mouse OVA antigen-exposed bronchial hypersensitivity model.

[0231] The primers and TaqMan probe used in the assay with ABI 7700 were designed based on the information on the sequence of each gene utilizing Primer Express (PE Biosystems). The 5' and 3' ends of the TaqMan probe were labeled with FAM (6-carboxy-fluorescein) and TAMRA (6-carboxy-N,N,N',N'-tetramethylrhodamine), respectively. The nucleotide sequences of oligonucleotides for the forward primer (F) , reverse primer (R), and TaqMan probe (TP) for each gene are shown below. The nucleotide sequences of the forward primer, TaqMan probe, and reverse primer used in the detection of each gene are indicated after probe ID, Accession No., symbol for each gene, and gene name, each of which are separated by //. The number in the parenthesis after each nucleotide sequence refers to the corresponding

SEQ ID NO. The 5' and 3' ends of the TaqMan probe were labeled with FAM (6-carboxy-fluorescein) and TAMRA (6-carboxy-N,N,N',N'-tetramethylrhodamine), respectively.
Genes whose expression levels varied in both humans and mice:

A1//NM_005409//SCYB11//"small inducible cytokine subfamily B (Cys-X-Cys), member 11 precursor"
CCTTGGCTGTGATATTGTGTGC(1642)
ACGCTGTCTTTGCATAGGCCCT(1643)
CTCAATATCTGCCACTTTCACTGC(1644)

A4//U21931//FBP1//"fructose-1,6-biphosphatase (FBP1) gene, exon 7"
TGTCTCACACAGCAGTACCCTG(1645)
TGCTGTGCACCTTACATTCCTAGAGAGCAG(1646)
GTGCCAAGCATTCTACAGCATT(1647)

A6//"NM_003856, NM_016232"//IL1RL1//interleukin 1 receptor-like 1
TGACTGAGGACGCAGGTGATT(1648)
CCAGGTCCTTCACGGTCAAGGATGA(1649)
GGGCTCCGATTACTGGAAACA(1650)

A9//U88317//ALOX15//arachidonate 15-lipoxygenase
CTGCAGACCTGGTGTCGAGAG(1651)
TCACTGAAATCGGGCTGCAAGGG(1652)
ACAGGAAACCCTCGGTCCTG(1653)

A10//D26579//ADAM8//a disintegrin and metalloproteinase domain 8 precursor
TGCTCCTCCGGTCACTGTG(1654)
CAGCCCACCCTTCCCAGTTCCTG(1655)
TTGATGACCTGCTTTGGTGC(1656)

A11//Y12653//diubiquitin//diubiquitin
TGTCCGGTCTAAGACCAAGGTTC(1657)
TGTGCAGGACCAGGTTCTTTTGCTGG(1658)
GGCTTCTCCGTGGCTTTAAGA(1659)

A19//NM_000120//EPHX1//epoxide hydrolase 1
TGAGGAGATCCACGACTTACACC(1660)
CGATAAGTTCCGTTTCACCCCACCTTTG(1661)
TCAGGTAGTTGGAGTTGAAGCCAT(1662)

A22//XM_051522//RDC1//G protein-coupled receptor
CGTGGACCGCTACCTCTCC(1663)
TCACCTACTTCACCAACACCCCCAGC(1664)
GGCGTACCATCTTCTTCCTGC(1665)

A24//NM_000598//IGFBP3//insulin-like growth factor-binding protein 3
CAGCGCTACAAAGTTGACTACGA(1666)
CCATATTCTGTCTCCCGCTTGGACTCG(1667)
CAGGTGATTCAGTGTGTCTTCCA(1668)

A25//m62402//IGFBP6//insulin-like growth factor-binding protein 6
CCAAGCAGGCACTGCCC(1669)
CCACAGGATGTGAACCGCAGAGACC(1670)
CGTGGTAGAGGTGCCTGGA(1671)

A26//NM_002964//S100A8//S100 calcium-binding protein A8
AGCTGGAGAAAGCCTTGAACTCT(1672)
TCCATGCCGTCTACAGGGATGACCTG(1673)

CTGAGGACACTCGGTCTCTAGCA(1674)

E1//NM_001843//CNTN1//contactin 1
GGTAGAGGAGAGCCCAGTATACCA(1675)
TGCTGCACCAAATGTGGCTCCTTC(1676)
GGCTTAAATGCCACTATGTAACCA(1677)

A57//NM_080657//cig5//vipirin
AAGAGGACATGACGGAACAGATC(1678)
AAGCACTAAACCCTGTCCGCTGGAAAGT(1679)
CCACAATTCTCACCCTCAATTAAGA(1680)

A59//u77643//SECTM1//secreted and transmembrane 1 precursor
TGGGACACCAGAGAAATAACAGAC(1681)
CACGCTGGAGGTTTCAGGTGCAGAAC(1682)
AGGCCAGAACCCAGTGTCAG(1683)

A68//NM_000096//CP//ceruloplasmin (ferroxidase)
TGGATGCTCAGCTGTCAGAATC(1684)
CATCTGAAAGCCGGTTTGCAAGCCT(1685)
TGTTACACTCCTGGACCTGGAA(1686)

B13//NM_012258//HEY1//hairy/enhancer-of-split related with YRPW motif 1
CAATGCACTGAGCCCTTCAG(1687)
CCCACGCAGGCTGCAAACCTTG(1688)
TCCGTCCCCCAAGGTCTATAG(1689)

B14//NM_033197//MGC14597//von Ebner minor salivary gland protein
GGCTTCCTTCAATGGCATGT(1690)
CAGCATTGACCGTCTGGAGTTTGACCT(1691)
GTCACCCTTGATGGCAGGAT(1692)

A77//NM_003355//UCP2//uncoupling protein 2
CCCTACTGCCACTGTGAAGTTTCT(1693)
CACAGCTGCCTGCATCGCAGATCT(1694)
AGCAGTATCCAGAGGAAAGGTGAT(1695)

A78//NM_012449//STEAP//six transmembrane epithelial antigen of the prostate
TGGAAAATGAAGCCTAGGAGAAAT(1696)
TGCTGGTCTCTCCCGTGTCCTTATGC(1697)
TCTGAAGGGCAGTCAAATTCATC(1698)

B21//"NM_016583, NM_130852"//LOC51297//LUNX protein; PLUNC (palate

lung and nasal epithelium clone); tracheal epithelium enriched protein

TGGCCACCGTCTCTATGTCA(1699)
CTCGGCATAAAGCTCCAAGTGAATACGCC(1700)
CCAGCCTCAACAGACTTGCA(1701)

B23//NM_006424//SLC34A2//"solute carrier family 34 (sodium phosphate), member 2"

CACTGTTCCCTCGACTGCTAACT(1702)
CTACAAGGAGAACATCGCCAAATGCCA(1703)
AAGATCCGGGAGGTGGAAATT(1704)

A83//u46569//AQP5//aquaporin 5 (exon4)

TTTCTGGGTAGGGCCCATC(1705)
CTGGCTGCCATCCTTTACTTCTACCTGCTC(1706)
ATGGCCACACGCTCACTCA(1707)

A84//AF030880//SLC26A4//"PDS(pendrin) mRNA, solute carrier family 26, member 4"

TTTGCCTCCTGAACTTCCACC(1708)
CTTGTTCTCGGAGATGCTGGCTGCAT(1709)
CCTACTGACACTGCAATAGCATAAGC(1710)

A89//x87159//SCNN1B//amiloride-sensitive sodium channel

ATTGATGAACGGAACCCCC(1711)
CACCCCATGGTCCTTGATCTCTTTGGA(1712)
TGCTGAGCTGCTTGTTAAGCC(1713)

A115//U70981//IL13RA2//"interleukin 13 receptor, α2"

TGCTCAGATGACGGAATTTGG(1714)
TGAGTGGAGTGATAAACAATGCTGGGAAGG(1715)
TGGTAGCCAGAAACGTAGCAAAG(1716)

Mouse genes;

A27//NM_019494 //SCYB11//"small inducible cytokine subfamily B (Cys-X-Cys), member 11 precursor"
TGGCAGAGATCGAGAAAGCTTC(1717)
ACCCGAGTAACGGCTGCGACAAAGTT(1718)
TCCAGGCACCTTTGTCGTTT(1719)

A30//NM_019395//FBP1//"fructose-1,6-biphosphatase (FBP1) gene, exon 7"
CCTCTGAAGATGTGCAGGAGTTC(1720)

CACAAAGCCAAGTGAAGGCCAGCC(1721)
CAGAATGGAGTAGCGTCACTTGA(1722)

A32//NM_010743//IL1RL1//interleukin 1 receptor-like 1
TCCTAGGTGGCCAGAGTTGTG(1723)
CCCAAGACCTCACTGATCACAACAGCA(1724)
CACCCGGAGTAACACCATTATCA(1725)

A35//NM_009660//ALOX15//arachidonate 15-lipoxygenase
TACCCCACCGCCGATTT(1726)
CACGCCCTTGGATCCCCCAATG(1727)
CCCAGCATTTGGCCAGG(1728)

A36//x13335//ADAM8//a disintegrin and metalloproteinase domain 8 precursor
GGCTCTCCAACCCCCTATTCTA(1729)
AGACAGTTTCTACCAACCAGCCCCCAAG(1730)
GCCTCTTTGGTTTCACTATGGG(1731)

A37//NM_0023137//diubiquitin//diubiquitin
TGACAAGGAAACCACTATCCACC(1732)
CCTGAAGGTGGTGAAGCCCAGTGATG(1733)
CCAGAAACAAGGGCAGCTCT(1734)

A45//NM_010145//EPHX1//epoxide hydrolase 1
CCTGGCTGCCTACATCTTAGAGAA (1735)
CTGGACCAAGTCAGAATACCGTGAACTGGA (1736)
TTAGTCAGCAGATCTTCCAGGGAG (1737)

A48//NM_007722//RDC1//G protein-coupled receptor
TGGGAGCATCTTCTTCCTCG (1738)
TGCATGAGCGTGGACCGCTATCTC (1739)
GCCGGTGAAGTAGGTGATGG (1740)

A50//NM_008343//IGFBP3//insulin-like growth factor-binding protein 3
GCAGGCAGCCTAAGCACCTA (1741)
CCTCCCAACCTGCTCCAGGAAACA (1742)
TGCTCCTCCTCGGACTCACT (1743)

A51//NM_008344//IGFBP6//insulin-like growth factor-binding protein 6
GGAGAGCAAACCCCAAGGAG (1744)
TGCCTCCCGCTCTCGTGACACAA (1745)

TCTTCTGCCGGTCTCTGTGG (1746)

A52//NM_013650//S100A8//S100 calcium-binding protein A8
GAGTGTCCTCAGTTTGTGCAGAA (1747)
CACCCACTTTTATCACCATCGCAAGGAA (1748)
CTTGTGGCTGTCTTTGTGAGATG (1749)

E2//NM_007727//CNTN1//contactin 1
CCCAGGAGGCCTGAGAATAGA (1750)
TGGTTCCGACAATCACAGCCCTATCTCT (1751)
GAATCGTCTTGGTCTGGATCGT (1752)

A64//NM_021384//cig5//vipirin
GACAGCTTCGATGAGCAGGTT(1753)
CCTTGACCACGGCCAATCAGAGCAT(1754)
CTGCACCACCTCCTCAGCTT(1755)

A66//AF210700//SECTM1//secreted and transmembrane 1 precursor
AAGGAGTCCAGGCCCAGC(1756)
CAGATGCTCAGGACAAACACTCAGGGAACT(1757)
TCCATGCAGCTTCCAGGAG(1758)

A72//NM_007752//CP//ceruloplasmin (ferroxidase)
ACAGCAACAACCTGTGCCTACA(1759)
TCAACCTGTTCCCTGCCACCCTAATTG(1760)
TGCAACCCAGCTTTCAGATG(1761)

B18//NM_010423//HEY1//hairy/enhancer-of-split related with YRPW motif 1
CACTCTCAGTCTCACGGATTTCA(1762)
CCAGTGTCGACCTGCGTAAGCGATC(1763)
TTCACAGGCACCAAGCTACTTTC(1764)

B19//U46068//MGC14597//von Ebner minor salivary gland protein
CACCCTGACCAAGATCCTTGA(1765)
TACACACTGCTGCCCAATGAGAATGGC(1766)
ACCCTTGCTCACAGACCACAT(1767)

A81//NM_011671//UCP2//uncoupling protein 2
GCATTGGCCTCTACGACTCTGT(1768)
CCTGCATGCTCTGAGCCCTTGGTGTA(1769)
GCCTGGAAGCGGACCTTTA(1770)

A82//NM_027399//STEAP//six transmembrane epithelial antigen of the prostate

AGTGACGATGTTACAAACCCAGAA(1771)
TGCTCGTCTCTCCCGAGTCCTTAGTCG(1772)
GAATTCCTGCGTGTGCTGAAG(1773)

B24//NM_011126//LOC51297//LUNX protein; PLUNC (palate lung and nasal epithelium clone); tracheal epithelium enriched protein
CAGCTTGCTCAATGGAGTCACT(1774)
AGGACATACCTTGCCCTGGATCAGCT(1775)
ACCAGGGTGACATCCAAACC(1776)

B26//NM_011402//SLC34A2//"solute carrier family 34 (sodium phosphate), member 2"
CTCCAGCACCTCTTCCTCCA(1777)
CCGAACCGTCAGCAATGAAGAAGCAA(1778)
TGTTAGCGCCCATGATGATG(1779)

A98//AF087654//AQP5//aquaporin 5 (exon4)
GAACCCAGCCCGATCTTTC(1780)
CCCTGCGGTGGTCATGAATCGGT(1781)
CCCAGAAGACCCAGTGAGAGG(1782)

A99//AF167411//SLC26A4//"PDS(pendrin) mRNA, solute carrier family 26, member 4"
GGTTCTTGCCTCCTGTCCTG(1783)
CATCTGTGGGCCTGTTTTCGGACATG(1784)
AATGGAAAAGGATGCAGCCA(1785)

A104//AF112186//SCNN1B//amiloride-sensitive sodium channel
TGGTCCTTATTGATGAGCGGA(1786)
TGACCACCCGGTGGTTCTCAATTTGTT(1787)
CGGGTTGCTGCTGTTGTG(1788)

A127//U65747//IL13RA2//"interleukin 13 receptor, α2"
ACACAGGGCCAGACTCAAAGAT(1789)
AACCTGAACCCACATTGAGCCTCCATG(1790)
GCACACACTTCTTTGTTCAGATCC(1791)

Genes whose expression levels tend to vary in both humans and mice:
Human genes;

A2//NM_006705//GADD45G//"growth arrest and DNA damage inducible, γ"
CCCAGCATCACCCTCCCCGA(1792)
CCCAGCATCACCCTCCCCGA(1793)
GCGTCACCACGTCGATCAG(1794)

A20//d00632//GPX3//glutathione peroxidase 3
GGACACATTAATATCACCCGGA(1795)
ACAGCCTCATTCATGGTTTCACGTGC(1796)
CCCGAGATTAGGAGTTGCTGTT(1797)

A53//NM_005168//ARHE//"ras homolog gene family, member E"
CCACAAAGCGGATTTCACACATGCC(1798)
CCACAAAGCGGATTTCACACATGCC(1799)
TCCTTTCGTAAGTCCGTAGCAACT(1800)

A67//NM_002305//LGALS1//β-galactosidase binding lectin precursor
TCCTGACGCTAAGAGCTTCGTGCTGAA(1801)
TCCTGACGCTAAGAGCTTCGTGCTGAA(1802)
AAGCGAGGGTTGAAGTGCA(1803)

C7//NM_005672//PSCA//prostate stem cell antigen
AGGCACTGCCCTGCTGTGCTACTCCT(1804)
AGGCACTGCCCTGCTGTGCTACTCCT(1805)
GCTCACCTGGGCTTTGCA(1806)

A93//NM_002659//UTPR//urokinase-type plasminogen receptor
ACACCACCAAATGCAACGAGG(1807)
TTGAAAATCTGCCGCAGAATGGCCG(1808)
TCCCCTTGCAGCTGTAACACTG(1809)

A96//j05070//MMP9//type IV collagenase
ACCTCGAACTTTGACAGCGAC(1810)
TGCCCGGACCAAGGATACAGTTTGTT(1811)
GAGGAATGATCTAAGCCCAGC(1812)

A120//S78825//ID1//"inhibitor of DNA-binding 1, dominant negative helix-loop-helix protein"
ATGAACGGCTGTTACTCACG(1813)
TGGAGATTCTCCAGCACGTCATCGACT(1814)
GATTCCGAGTTCAGCTCCAA(1815)

Mouse genes;

A28//NM_011817//GADD45G//"growth arrest and DNA-damage-inducible, γ"
GCATTGCATCCTCATTTCGAAT(1816)
TGAGGACACATGGAAGGACCCTGCC(1817)
CCTCGCAGAACAAACTGAGCTT(1818)

A46//u13705//GPX3//glutathione peroxidase 3

AGAAGAACTTGGGCCATTTGG(1819)
TTCTGGGCTTCCCTTCCAACCAATTTG(1820)
TCTCGCCTGGCTCCTGTTT(1821)

A60//NM_028810//ARHE//"ras homolog gene family, member E"
GGGATGGTGCCCCTAGACTAG(1822)
CTGTCGTCTGGTGCCACTTCCTTCAA(1823)
GGGTTTTGCCAGAACAGCATT(1824)

A71//NM_008495//LGALS1//β-galactosidase-binding lectin precursor
ACAGCAACAACCTGTGCCTACA(1825)
CCCATGGAGACGCCAACACCATTG(1826)
CCCATCTTCCTTGGTGTTACA(1827)

C8//AW209486//PSCA//prostate stem cell antigen
CATCCCATCTCAGCCTTTACCA(1828)
CCTACTCTCCAGGGCCTGAGCCAGTG(1829)
GCCCTACCAAGTTTTGCTCAGA(1830)

A108//NM_011113//UTPR//urokinase-type plasminogen receptor
CAATGGTGGCCCAGTTCTG(1831)
AGCTTTCCACCGAATGGCTTCCAGTGT(1832)
GGGTATTGTTCCCCTCACAGC(1833)

A111//NM_013599//MMP9//type IV collagenase
CCATGCACTGGGCTTAGATCA(1834)
AGCGTGCCGGAAGCGCTCAT(1835)
TCGAGGTAGCTATACAGCGGG(1836)

A132//U43884//ID1//"inhibitor of DNA-binding 1, dominant negative helix-loop-helix protein"
CGACATGAACGGCTGCTACTC(1837)
CGCCTCAAGGAGCTGGTGCCC(1838)
CTTGCTCACTTTGCGGTTCTG(1839)

Genes whose expression levels varied in humans:
Human genes;

A3//NM_000625//NOS2A//"nitric oxide synthase 2A (inducible, hepatocytes)"
ACCCTGAGCTCTTCGAAATCC(1840)
TTAGCTCCAGTTCCCGAAACC(1841)
TTAGCTCCAGTTCCCGAAACC(1842)

A5//NM_005101//ISG15//"interferon-stimulated protein, 15 kDa"

GGGACCTGACGGTGAAGATG(1843)
CTGACACCGACATGGAGCTGCTCAG(1844)
GCCAATCTTCTGGGTGATCTG(1845)

A8//NM_003956//CH25H//cholesterol 25-hydroxylase
ACGTGGTCAACATCTGGCTTTC(1846)
TCCGGCTACAACTTCCCTTGGTCCA(1847)
GGAGCGAAGTTGCAGTTAAAGTG(1848)

A12//U19557//SERPINB4 (SCCA2)//"serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4"
AGCCACGGTCTCTCAG(1849)
AAGGCCTTTGTGGAGGTCACTGAGGAGGGA(1850)
GCAGCTGCAGCTTCCA(1851)

A13//NM_002575//SERPINB2//"serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2"
ATGGTCCTGGTGAATGCTGTCTA(1852)
TGTAAACTCGGCTCAGCGCACACCT(1853)
GCTTTTCACGCAAGTACATCATCT(1854)

A15//NM_000433//NCF2//neutrophil cytosolic factor 2
TAGCATTGGCCACGAGCAT(1855)
TGAGCCCAGACATTCCAAAATCGACA(1856)
GATCACCACTGGCTCATATAGCTTCT(1857)

A23//NM_000435//NOTCH3//Notch homolog 3
ACTTTGCCAACCGTGAGATCA(1858)
TCCTGGTGCAGTCTCTCCTGGGCTA(1859)
ATCCAGCAAGCGCACGAT(1860)

B1//NM_022168//MDA5//melanoma differentiation associated protein-5
GACCCCAGAATTCAAGGAACTTT(1861)
CAAGCCTGGCCACATTTGCAGATGA(1862)
GCCTTTGTGCACCATCATTGT(1863)

B2//NM_052942//GBP5//guanylate binding protein 5
AAAATTGGCTGGCAGAGCAA(1864)
CTGCACAGCTCAGCACAACATTCCAA(1865)
CGTGCTGGAGCTCACTGAGA(1866)

B3//NM_018584//PRO1489//hypothetical protein PRO1489
AGAGGAGCCCAGAGCCTTCT(1867)
TCATCTGTCTCCCGGCCTGATACCA(1868)

CCCACGATGAAATCAACAACCT(1869)

C2//NM_032323//MGC13102//hypothetical protein MGC13102
CCAGTCGGTCCAGCTCTTTATT(1870)
TCAACCTGGCCGTGCTTTCCACTT(1871)
TCAACCTGGCCGTGCTTTCCACTT(1872)

A54//NM_003238//TGFB2//"transforming growth factor, β2"
CCTGAACAACGGATTGAGCTATATC(1873)
CCCAGCGCTACATCGACAGCAAAGT(1874)
AACAGCATCAGTTACATCGAAGGA(1875)

A55//NM_001539//DNAJA1//"DnaJ (Hsp40) homolog, subfamily A, member 1"
CCAAGTAGAACTGGTGGACTTTGA(1876)
CCAAATCAGGAAAGACGGCGCCA(1877)
CATCCTCATATGCTTCTCCATTGT(1878)

A56//NM_003032//SIAT1//"sialyltransferase 1 (β-galactoside α-2,6-sialytransferase)"
ACGCAGTCCTGAGGTTTAATGG(1879)
CACCCACAGCCAACTTCCAACAAGATGT(1880)
GCACAAAAACTACCATTCGCCT(1881)

B9//NM_013324//CISH //cytokine-inducible SH2-containing protein
TGTGCATAGCCAAGACCTTCTC(1882)
CCAATACCAGCCAGATTCCCGAAGGTA(1883)
CTGGCATCTTCTGCAGGTGTT(1884)

A69//NM_006408//AGR2//anterior gradient 2 homolog (Xenepus laevis)
CAGTTTGTCCTCCTCAATCTGGTT(1885)
TGTCCCCAGGATTATGTTTGTTGACCCA(1886)
TTCCAGTGATATCGGCTCTAACTGT(1887)

A70//NM_002443 NM_138634//MSMB//"microseminoprotein, β-, isoform a, b"
ACCTGTCTATAAGGAGTCCTGCTTATC(1888)
CAATGAATGTTCTCCTGGGCAGCGTT(1889)
AAGTCACGAAGGTGGCAAAGAT(1890)

B11//NM_024539//FLJ23516//hypothetical protein FLJ23516
CTGCTCGAAGGCTACGGAAT(1891)
TCTGCCTTTAATTGCCTCTGCTTCCTG(1892)
TGCGTAGTTGAAGCCTTCCA(1893)

B15//NM_002247//KCNMA1//"potassium large conductance calcium-activated channel, subfamily M, α member 1"
CCGTGCCAGCAACTTTCATT(1894)
CCAAAGTGTCCATATTGCCTGGTACGCC(1895)
CCCTTAAATCAGCCCGACTTAA(1896)

C5//NM_018050//FLJ10298//hypothetical protein FLJ10298
CGAGGAAGCCTGTCCATTGA(1897)
TGACCAGAAATTTGCCAAGCCAAGAGTT(1898)
GCTTGTGAAAATTGGCCATGT(1899)

A75//NM_003246//THBS1//throbospondin 1
TCCAGCATGGTCCTGGAACT(1900)
TCTTCAGTCACTTTGCGGATGCTGTCCT(1901)
TGAACTCCGTTGTGATAGCATAGG(1902)

A76//NM_005688//ABCC5//"ATP-binding cassette, sub-family C, member 5"
GGACACTGCACAGCATCGAT(1903)
CCGCAGATTCCAACCAGTTTACCCTCTT(1904)
CGAAGGTTCCACTGATTGCAA(1905)

E3//NM_016354//SLC21A12//"solute carrier family 21 (organic anion transporter), member 12"
GCGTCACCTACCTGGATGAGA(1906)
TACATTGCCATCTTCTACACAGCGGCC(1907)
GCCCATTTCCGTGTAGATATTCA(1908)

E4//NM_012434//SLC17A5//"solute carrier family 17 (anion/sugar transporter), member 5"
TGCCACTATTCCAGGAATGGTT(1909)
CACGGTTTGCCATTCTCCAACAGTGTTA(1910)
CTTCACCTTTGGCGAATAGTGTAA(1911)

A87//x52947//GJA1//"cardiac gap junction protein, connexin 43"
GGTTACTGGCGACAGAAACAATTC(1912)
CGCAATTACAACAAGCAAGCAAGTGAGC(1913)
TGCCCCATTCGATTTTGTTC(1914)

A90//d28137//BST2//BST2
CAGTGATGGAGTGTCGCAATG(1915)
CATCTCCTGCAACAAGAGCTGACCGA(1916)
CACATCCTGAAAGCCCTTCTG(1917)

A94//j04164//IFI9-27//interferon-inducible protein9-27
CCTCTTCTTGAACTGGTGCTGT(1918)
TGGGCTTCATAGCATTCGCCTACTCC(1919)
CCATCTTCCTGTCCCTAGACTTC(1920)

A97//m24283//ICAM1//major group rhinovirus receptor (ICAM1)
GCTGACGTGTGCAGTAATACTGG(1921)
CAGACAGTGACCATCTACAGCTTTCCGG(1922)
TTCTGAGACCTCTGGCTTCGT(1923)

A113//D13666//OSF-2//osteoblast specific factor 2 (fasciclin I-like)
AGCAAACCACCTTCACGGATC(1924)
AATTAGGCTTGGCATCTGCTCTGAGGCC(1925)
GGTGCCAGCAAAGTGTATTCTCC(1926)

A114//D31784//CDH-6//"cadherin 6, type 2 preproprotein"
CGCAGTTCTGTAGTTGAGTTTCAAGG(1927)
TTAGCAGGGTTGATGTGGAGCGTGAAG(1928)
ACCAAGAACAGAATGCCCAGG(1929)

A116//U21049//DD96//"epithelial protein upregulated in carcinoma, membrane associate"
GCCTTTGCAGTCAACCACTTCTG(1930)
ATGATCCTGACCGTCGGAAACAAGGC(1931)
TCTGTTCCCACCAGGACTCCAT(1932)

A117//X87212//CTSC//cathepsin C
TCTCAGACCCCAATCCTAAGCC(1933)
TCTTGTAGCCAGTATGCTCAAGGCTGTGAA(1934)
CTGCAATAAGGTATGGGAAGCC(1935)

A118//U17077//BENE//BENE protein
TGCCCGAGCTGATATTTGG(1936)
TAGCCGCCACCCACATAGTATACCCCTT(1937)
CATACATCACCCATCCTTGCAG(1938)

A121//AI979079//FLJ10261//hypothetical protein FLJ10261
TTTGTCACTGAGCTCCGAAGG(1939)
TAGCTGTCAGAGCCAAAGACATCGGAATCT(1940)
TCCCAATGCCTCTGAGGATATT(1941)

A122//M87434//OAS2//2'-5'-oligoadenylate synthetase 2 (69-71 kD)
CATCAGGAACATCCTGCTGCA(1942)

CAGCTCCAATCAGCGAGGCCAGTAATCT(1943)
CACATTATTGGTTGGGTCAACTGG(1944)

A123//AB032953//Odz2//"odd Oz/ten-m homolog 2 (Drosophila, mouse)"
AGGCATGGTCAATGCCAGGT(1945)
TCATGACAACAGCTTCCGCATCGCAA(1946)
AGTCTCACTTATGACGGGCTTGATG(1947)

A124//X82693//E48//"lymphocyte antigen 6 complex, locus D"
AAGCATTCTGTGGTCTGCCC(1948)
CTCGCTTCTGCAAGACCACGAACACA(1949)
TTCACCAGATTCCCCCTCAGAG(1950)

A137//AF061812//KRT16//"keratin type 16 gene, exon 8"
CACCATTGAGAATGCGCAG(1951)
TTTTGCAGATTGACAATGCCAGGCTG(1952)
ACTTGGTCCTGAAGTCATCGG(1953)

Mouse genes;

A29//m84373//NOS2A//"nitric oxide synthase 2A (inducible, hepatocytes)"
TGACGGCAAACATGACTTCAG(1954)
AATTCACAGCTCATCCGGTACGCTGG(1955)
GCCATCGGGCATCTGGTA(1956)

A38//NM_009126//SERPINB4 (SCCA2)//"serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4"
ATGACCTCCCAATTCCATTGG(1957)
ACATGGGAATGGTCGATGCCTTTGA(1958)
ACCAGAGAAGTCAGCCTTCTGTG(1959)

A39//NM_011111//SERPINB2//"serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2"
CACATGAGGTTTTGTAGCATGAACT(1960)
AGCCTCAGAATTGCATCTTCAAGTGCCA(1961)
GCACTGAAGACTGCTATACAATTGC(1962)

A41//NM_010877//NCF2//neutrophil cytosolic factor 2
ACCACCTCCTAATTCTAGCCCC(1963)
AGTTGTCACCAGGTCACAAGCAAAAAGAGC(1964)
CATGTAAGGCATAGGCACGCT(1965)

B5//AA959954//MDA5//melanoma differentiation associated protein-5
GAGAGCAAATGTGGACTCAGCTAGT(1966)

TGTAGCCCGAGATCACCCACAGAGAAC(1967)
AATGCCCATGAGGTATTGTCCTA(1968)

B6//NM_010259//GBP5//guanylate binding protein 5
GCAGCAAATAGAGCATTGGC(1969)
AGCATGAGATGCTGATGGAACAGAAGGA(1970)
TGCTCCATCTTCTCAGTCAGC(1971)

C4//NM_024246//MGC13102//hypothetical protein MGC13102
GGGCTGGCGAGATATTGAAC(1972)
CCATTCAAAGAGGATGCCAACCTGCTC(1973)
CGCTCGATGCACTGTAGATCA(1974)

A61//NM_009367//TGFB2//"transforming growth factor, β2"
TTACCCTAAGCGAGAAAGTGCAA(1975)
CGCAGCCAACGCGCCCA(1976)
CCTTAACCCCTGTGGAACAACA(1977)

A62//NM_008298//DNAJA1//"DnaJ (Hsp40) homolog, subfamily A, member 1"
TGTCTAGTTATATGAAGTGAACCAATTGTG(1978)
TGCCTTTGCATTGTATTGCCTCAGCC(1979)
CGAAATGTATTATGCCACCTTCTAGTAA(1980)

A63//D16106//SIAT1//"sialyltransferase 1 (β-galactoside α-2,6-sialytransferase)"
GGGTTACCTGCCCAAAGAGAC(1981)
TTCAGAACCAAGGCTGGGCCTTGG(1982)
CAGAAGACACGACGGCACAC(1983)

B10//NM_009895//CISH //cytokine-inducible SH2-containing protein
CAGTGCCCGCAGCTTACAA(1984)
CTGTGTCGGCTAGTCATCAACCGTCTGG(1985)
TCGGAGGTAGTCGGCCATAC(1986)

B16//NM_023270//FLJ23516//hypothetical protein FLJ23516
TCGCAGTGAGACTGCATCATC(1987)
CTTCAGTACAAGGAGCAGATGAGCCACCTC(1988)
TTTGCTGACTGCGCATGTTC(1989)

B20//NM_010610//KCNMA1//"potassium large conductance calcium-activated channel, subfamily M, α member 1"
TGGTAACGTGGACACCCTTGA(1990)
TAATGATTGCTCCACCAGTTTCCGTGC(1991)

GTTGGCGGCTGCTCATCTT(1992)

C6//NM_026345//FLJ10298//hypothetical protein FLJ10298
GTCCTCTGCATGCTAGGCAAG(1993)
AGCCATCCCTCAGTCCAACCACTTTCTG(1994)
ACCCTTCTTCTCTTCCTCTTTAAAAAA(1995)

DOCID: <EP_____1394274A2_I_>

A79//NM_011580//THBS1//throbospondin 1
GGTGCTGCAGAATGTGAGGTT (1996)
AGGCTGCTCCAGCTCTACCAACGTCCT (1997)
AACCGTTCACCACGTTGTTGT (1998)

A80//NM_013790//ABCC5//"ATP-binding cassette, sub-family C, member 5"
TGGAGGCTGCATCAAGATTG (1999)
TCAGTGGCACTGTCAGATCAAACCTGG (2000)
TCTTCCGTGTACTGGTTGAAAGG (2001)

A102//M61896//GJA1//"cardiac gap junction protein, connexin 43"
CGAGCAAAACTGGGCGAA (2002)
ACAGCGCAGAGCAAAATCGAATGGG (2003)
ATGGTGCTTCCGGCCTG (2004)

A109//AK003407//IFI9-27//interferon-inducible protein9-27
AGGTGTCGGTGCCTGACC (2005)
TGGTCTGGTCCCTGTTCAATACACTCTTCA (2006)
GCCCAGGCAGCAGAAGTTC (2007)

A112//m31585//ICAM1//major group rhinovirus receptor (ICAM1)
AGTCCGCTGTGCTTTGAGAAC (2008)
TGGCACCGTGCAGTCGTCCG (2009)
CCGGAAACGAATACACGGTG (2010)

A125//D13664//OSF-2//osteoblast specific factor 2 (fasciclin I-like)
TAGCCCAATTAGGCTTGGCATCC (2011)
TAGCACCTGTGAACAATGCGTTCTCTGATG (2012)
TAAGAAGGCGTTGGTCCATGCT (2013)

A126//D82029//CDH-6//"cadherin 6, type 2 preproprotein"
TTTAAGACCCCCGAGTCCTCTC (2014)
CCAATTGGCAGGATCAAAGCCAGTGA (2015)
CTCCGCATTTTCTCCCACATC (2016)

A128//AW01791//DD96//"epithelial protein up-regulated in carcinoma,

membrane associate"
GATGCAAGGCCTCATTGCTG(2017)
CGCTGTGTTCTTGGTCCTTGTTGCAA(2018)
AGAAGTGGTTGACGGCGAAGAC(2019)

A129//U74683//CTSC//cathepsin C
TCTCAGACACCAATCCTGAGTC(2020)
TCTTGCAGCCCCTATGCCCAAGGTTGTGAT(2021)
CTGCAATGAGGTATGGGAATCC(2022)

A130//BC012256//BENE//BENE protein
CGGGTTCTGGGTGTGGACT(2023)
CTGCTACACACGTCGCATACCCCTTG(2024)
CATACAGCACCCATCCCTGC(2025)

A133//BC006062//FLJ10261//hypothetical protein FLJ10261
CGGCATCTGGTATAACATCCTCA(2026)
AGGTGTTGGGAAGCTGGCTGTCATCA(2027)
GATGAAGTCAGACGTGAAGGAGATC(2028)

A135//NM_011856//Odz2//"odd Oz/ten-m homolog 2 (Drosophila, mouse)"
GAATGATCAACGCCAGGTTTG(2029)
ACCTATCACGACAATAGCTTCCGCATTGC(2030)
CGCTAATGACGGGTTTGATGC(2031)

A136//X53782//E48//"lymphocyte antigen 6 complex, locus D"
GGTCTGCCCGTCCAACTTC(2032)
TTCTGCAAAACCGTCACCTCAGTGGAG(2033)
TCACCAGGTTCCCATTCAGAG(2034)

A138//AF053235//KRT16//"keratin type 16 gene, exon 8"
TCAAGACCATTGAGGACCTGA(2035)
ACACGATCACCTACTCACTCCTCAAGCA(2036)
AGCCTGGCATTGTCAATCTG(2037)

Genes whose expression levels tend to vary in humans:
Human genes;

A16//NM_002997//SDC1//syndecan 1
TGGTGGGTTTCATGCTGTACC (2038)
TGAAGAAGAAGGACGAAGGCAGCT (2039)
GCATAGAATTCCTCCTGTTTGGTG (2040)

A21//NM_024090//LCE//hypothetical protein MGC5487
TCTCTGACCCTTGCAGTCTTCA (2041)

CATTTTGATGACCAAAGGCCTGAAGCA (2042)
GAATTTGCTGACAGGTCCATTG (2043)

A88//u17986//SLC6A8//SLC6A8
TCCTACTACTTCCGTTTCCAAAGG (2044)
CCTCTGTTGTGCCCTCTGCTTTGTCAT (2045)
CTCACATCAGTCACCATGGAGAG (2046)

Mouse genes;

A42//NM_011519//SDC1//syndecan 1
GGCTTTCATGCTGTACCGGAT (2047)
TGGAGGAGCCCAAACAAGCCAATG (2048)
AGGCGTAGAACTCCTCCTGCTT (2049)

A47//NM_130450//LCE//hypothetical protein MGC5487
AGCTGTACTTTGATTGCAGGTCAA (2050)
CTCACCAGTTGTCCATGTCCACCCAC (2051)
GGACCAATCAGCTAGGACAACTTG (2052)

Genes whose expression levels varied in mice:
Human genes;

A17//NM_000667//ADH1A//"class I alcohol dehydrogenase, α subunit"
TTTCCCTTGTGGCAGTCTTCA (2053)
CCTCTACCCTACATGATCTGGAGCAACAGC (2054)
TTGGAAAGCCCCCAAATGT (2055)

A58//NM_014375//FETUB//fetuin B
CCGAGTCTCTTGCGAAATACAA(2056)
ACAACCCACTGGCTAGAAGCCCTGGT(2057)
CGGAGGACTGAAGTGAACAGCT(2058)

B22//NM_014585//SLC11A3//"solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3"
AACCGCCAGAGAGGATGCT(2059)
TGGATCCTTGGCCGACTACCTGACCT(2060)
CACATCCGATCTCCCCAAGTA(2061)

A119//V01512//c-fos//cellular oncogene c-fos (complete sequence)
GGCAAGGTGGAACAGTTATCTCC(2062)
TCCGAAGGGAAAGGAATAAGATGGCTGCA(2063)
AGTGTATCAGTCAGCTCCCTCCTC(2064)

Mouse genes;

A43//NM_007409//ADH1A//"class I alcohol dehydrogenase, α subunit"

TGTGGTGTAAGCGTCGTCGTA(2065)
CCAATGCCCAGAACCTCTCCATGAAC(2066)
CGCCAAATATTGCTCCCTTC(2067)

A44//NM_008030//FMO3//Flavin-containing Monooxygenase 3
CTTGCAGCCCCTACCAGTTC(2068)
CCCGGAACGCCATCCTAACACAGTG(2069)
TGACGACACGCGTCTTCATAG(2070)

A65//NM_021564//FETUB//fetuin B
CTCGTCAAAGTCACCAAGGCTAT(2071)
CCATGTACCAAATCCCAGGCCAGCT(2072)
AATACCAACGGGCTCAGAGTCA(2073)

B25//NM_016917//SLC11A3//"solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3"

CTATTCTCAGGACTAGCCCAGCTT(2074)

TCCAGGCATGAATACGGAGATCACACA(2075)

CCTAGAACGGATATCTTCAAATGGA(2076)

A131//V00727//c-fos//cellular oncogene c-fos (complete sequence)

CCTGAAGAGGAAGAGAAACGGAG(2077)

CGAAGGGAACGGAATAAGATGGCTGC(2078)

CGATTCCGGCACTTGGC(2079)

[0232] The total RNAs extracted by the method described above were treated with DNase (Nippon Gene Co., Ltd.). Then, the cDNAs prepared by reverse transcription were used as templates. The primer used was random hexamer (GIBCO BRL). A plasmid clone for each gene, which contained the nucleotide sequence region amplified with the pair of primers, was prepared for a standard curve to determine the copy number. A dilution series of the plasmid was used as templates in the PCR assay. The composition of the reaction solution used to monitor PCR amplification was the same as that shown in Table 39.

[0233] Furthermore, similar quantitative analyses for the β-actin gene and the glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene as internal standards for correction were carried out to correct the difference of cDNA concentration in a sample. The copy number of the gene of interest was determined by correcting based on the determined copy numbers for the genes.

[0234] The nucleotide sequences of primers and probes used in the assays for human and mouse β-actin, and human and mouse GAPDH, are the same as shown in Example 6 (human: SEQ ID Nos: 7 to 12) and Example 9 (mouse: SEQ ID NOs: 18 to 23). The expression levels (copy/ng RNA) of the respective genes corrected with the level of β-actin are shown in Figs 7 to 31 (altered in both human and mouse) and Figs 32 to 69 (altered in human). In the OVA-administered group, the respective genes showed significant variations in expression levels. Specifically, the expression levels of genes belonging to groups (A) and (B) were confirmed to be increased and decreased, respectively.

6. Determination of the localization of each mRNA in the lung of OVA antigen-exposed bronchial hypersensitivity model by in situ hybridization (hereinafter referred to as "ISH")

[0235] A32/IL-1R-1, A36/ADAM 8, A37/diubiqutin, A42/SDC1, A50/IGFBP3, and A129/CTSC were analyzed for the localization pattern. After perfusion fixation with 10% buffered neutral formalin, the pulmonary tissues were removed from three mice from the naive group and each of the other three groups (S-Sal group, Pred group and S-OVA group) 24 hours after the final exposure to the antigen. The tissues were fixed with 10% buffered neutral formalin, and then embedded in paraffin to prepare tissue blocks.

[0236] All paraffin blocks from the mouse lung samples were sliced into 3 μm sections. Then, the sections were treated with hematoxylin for nuclear staining. Among them, sections exhibiting good tissue morphology were selected from a single individual each of the S-Sal group and S-OVA group for carrying out ISH. The nucleotide sequences of the ISH probes are shown in the following SEQ ID NOs:

CTSC (SEQ ID NO: 2080, 2081);

IL-1 receptor 1 (SEQ ID NO: 2082);

ADAM8 (SEQ ID NO: 2083);

Diubiquitin (SEQ ID NO: 2084);

SDC1 (SEQ ID NO: 2085);

and

IGFBP3 (SEQ ID NO: 2086).

[0237] The paraffin sections of mouse lung tissues from the S-Sal group and the S-OVA group were rehydrated by deparaffinization (washed with water after treatment with xylene, 100%, 90%, 80%, and 70% alcohol). Then, the sections were treated with the ISH probe described above. After the staining, the sections were treated for nuclear staining. The conditions used for the ISH experiments are described below. The ISH result is shown in Table 158.

Probe concentration: 250 ng/ml
Hybridization temperature: 60°C
Duration of hybridization: 6 hours
Post-hybridization wash: 0.1x SSC/70°C /6 minutes/3 times
Coloring reagents: NBT/BCIP
Duration of color development: 7 hours

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site	constituting cell	A32;IL-1R-1			A36;ADAM 8			A37;diubiquitin			A42;SDC1			A50;IGFBP3			A129;CTSC		
		Naive	S-Sal	S-OVA	Naive	S-Sal	S-OVA	Naive	S-Sal	S-OVA	Naive	S-Sal	S-OVA	Naive	S-Sal	S-OVA	Naive	S-Sal	S-OVA
bronchial branch	epithelial cell	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ND	-	-
	goblet cell	-	-	-	-	-	++	+	+	++	+/-	+	+	+	+	++	ND	-	-
	lymphocyte	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	ND	-	-
	macrophage	-	-	++	-	-	-	-	-	-	-	-	-	-	-	-	ND	-	+
	smooth muscle cell	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ND	-	-
bronchiole	epithelial cell	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ND	-	-
	Clara cell	-	-	-	-	-	-	-	+	+	-	+	+	-	-	-	ND	-	-
	goblet cell	-	-	-	-	-	-	-	+	+	-	+	+	-	-	-	ND	-	-
	lymphocyte	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	ND	-	-
	macrophage	-	-	++	-	-	-	-	-	-	-	-	-	-	-	-	ND	-	+
	smooth muscle cell	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ND	-	-
alveolus (alveolar duct)	type I alveolar epithelial cell	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ND	-	-
	type II alveolar epithelial cell	-	-	-	-	-	++	-	-	++	-	-	-	+	+	++	ND	-	-
	macrophage	-	-	++	-	-	-	-	-	-	-	-	-	-	-	-	ND	-	+
	alveolar macrophage	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ND	-	+
	endothelial cell	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ND	-	-
	fibroblast	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ND	-	-
Invasive cell		x	x	-	x	x	-	x	x	++*	x	x	++*	x	x	++*	ND	x	-

x : invasive cell
*: only plasma cells were stained

Claims

1. A method of testing for bronchial asthma or chronic obstructive pulmonary disease, which comprises the steps of:

   (1) determining the expression level of a marker gene in a biological sample from a subject;
   (2) comparing the expression level determined in step (1) with the expression level of the marker gene in a biological sample from a healthy subject; and
   (3) judging the subject to have bronchial asthma or chronic obstructive pulmonary disease when the result of the comparison in step (2) indicates that (i) the expression level of the marker gene in the subject is higher than that in the control when the marker gene is a gene according to (a) or (ii) when the expression level of the marker gene in the subject is lower than that in the control when said marker gene is a gene according to (b);

   wherein the marker gene is any one selected from the group according to (a) or (b):

   (a) a group of genes whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13, and comprise any one of the nucleotide sequences of SEQ ID NOs: 25 to 310;
   (b) a group of genes whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13, and comprise any one of the nucleotide sequences of SEQ ID NOs: 311 to 547.

2. The testing method according to claim 1, wherein the biological sample is a respiratory epithelial cell.

3. The testing method according to claim 1, wherein the gene expression level is measured by PCR analysis of the cDNA.

4. The testing method according to claim 1, wherein the gene expression level is measured by detecting the protein encoded by the marker gene.

5. A reagent for testing for bronchial asthma or chronic obstructive pulmonary disease, wherein the reagent comprises a polynucleotide comprising the nucleotide sequence of a marker gene, or an oligonucleotide having at least 15 nucleotides and comprising a nucleotide sequence complementary to the complementary strand of the nucleotide sequence of the marker gene, and wherein, the marker gene is any one selected from the group according to (a) or (b) in claim 1.

6. A reagent for testing for bronchial asthma or chronic obstructive pulmonary disease, wherein the reagent comprises an antibody that recognizes a protein encoded by a marker gene, and wherein the marker gene is any one selected from the group according to (a) or (b) in claim 1.

7. A method of screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, wherein the marker gene is any one selected from the group according to (a) or (b) in claim 1, and wherein the method comprises the steps of:

   (1) contacting a candidate compound with a cell expressing the marker gene;
   (2) measuring the expression level of said gene; and
   (3) selecting a compound that decreases the expression level of a marker gene belonging to group (a) or increases the expression level of a marker gene belonging to group (b), as compared to that in a control with which the compound has not been contacted.

8. The method according to claim 7, wherein the cell is a respiratory epithelial cell or a goblet cell.

9. The method according to claim 8, which comprises the step of culturing the respiratory epithelial cells under the condition in which culture medium is removed from the apical side of said cells and the culture medium is supplied from the basolateral side of the cells.

10. A kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease, wherein the kit comprises (i) a polynucleotide comprising the nucleotide sequence of a marker gene, or an oligonucleotide having at least 15 nucleotides and comprising a nucleotide sequence that is complementary to the complementary strand of the polynucleotide, and (ii) a cell expressing the marker gene, and wherein the marker gene is any one selected from the group according to (a) or (b) in claim 1.

)OCID: <EP_____1394274A2_I_>

11. A kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease, wherein the kit comprises (i) an antibody that recognize a protein encoded by a marker gene, and (ii) a cell expressing the marker gene, wherein the marker gene is selected from the group according to (a) or (b) in claim 1.

12. The kit according to claim 10 or 11, which further comprises a cell-supporting material to culture respiratory epithelial cells under conditions in which the culture medium is supplied from the basolateral side of the cells.

13. The kit according to claim 12, which further comprises respiratory epithelial cells.

14. An animal model for bronchial asthma or chronic obstructive pulmonary disease, wherein the animal is a transgenic nonhuman vertebrate wherein the expression level of a marker gene, or a gene functionally equivalent to the marker gene, has been increased in the respiratory tissue, wherein the marker gene is any one selected from the group according to (a) in claim 1 or the following (A):

(A) a group of genes whose expression levels increase in the lung of an animal model for bronchial hypersensitivity induced by an exposure to the ovalbumin antigen, wherein the genes comprise any one of the nucleotide sequences of SEQ ID NOs: 954 to 1174.

15. The animal model according to claim 14, wherein the nonhuman vertebrate is a mouse.

16. An animal model for bronchial asthma or chronic obstructive pulmonary disease, wherein the animal is a transgenic nonhuman vertebrate wherein the expression level of a marker gene, or a gene functionally equivalent to the marker gene, has been decreased in the respiratory tissue, wherein the marker gene is any one selected from the group according to (b) in claim 1 or the following (B) :

(B) a group of genes whose expression levels decrease in the lung of an animal model for bronchial hypersensitivity induced by an exposure to the ovalbumin antigen, wherein the genes comprise any one of the nucleotide sequences of SEQ ID NOs: 1376 to 1515.

17. The animal model according to claim 16, wherein the nonhuman vertebrate is a mouse.

18. A method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease, which comprises the step of administering to a mouse any one of (i) to (iv):

(i) a polynucleotide comprising the nucleotide sequence constituting any one of the genes selected from the gene group according to (A) in claim 14;
(ii) a protein encoded by a polynucleotide comprising the nucleotide sequence constituting any one of the genes selected from the gene group according to (A) in claim 14;
(iii) an antisense nucleic acid of a polynucleotide comprising the nucleotide sequence constituting any one of the genes selected from the gene group according to (B) in claim 16, a ribozyme, or a polynucleotide that suppresses the expression of a gene through an RNAi (RNA interference) effect; and
(iv) an antibody that binds to a protein encoded by a polynucleotide comprising the nucleotide sequence constituting any one of the genes selected from the gene group according to (B) in claim 16, or a fragment comprising an antigen-binding region thereof.

19. An inducer that induces bronchial asthma in a mouse, wherein said inducer comprises as an active ingredient any one of (i) to (iv) in claim 18.

20. A method of screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease comprising the steps of:

(1) administering a candidate compound to an animal subject,
(2) assaying the expression level of the marker gene in a biological sample obtained from the animal subject, and
(3) selecting a compound that decreases the expression level of a marker gene belonging to group (a) or (A) , or a compound that increases the expression level of a marker gene belonging to group (b) or (B) , as compared to that in a control with which the candidate compound has not been contacted,

wherein the marker gene is any one selected from the group consisting of (a) or (b) in claim 1, (A) in claim 14, and (B) in claim 16, or a gene functionally equivalent to said marker gene.

21. A method of screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease comprising the steps of:

(1) contacting a candidate compound with a cell into which a vector has been introduced, wherein the vector comprises a transcriptional regulatory region of a marker gene and a reporter gene that is expressed under the control of the transcriptional regulatory region,
(2) measuring the activity of the reporter gene, and
(3) selecting a compound that decreases the expression level of the reporter gene when the marker gene belongs to group (a), or a compound that increases the expression level of the reporter gene when the marker gene belongs to group (b) , as compared to that in a control with which the candidate compound has not been contacted,

wherein the marker gene is any one selected from the group according to (a) or (b) in claim 1, or a gene functionally equivalent to the marker gene.

22. A method of screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease comprising the steps of:

(1) contacting a candidate compound with a protein encoded by a marker gene,
(2) measuring the activity of the protein, and
(3) selecting a compound that decreases the activity when the marker gene belongs to group (a) , or a compound that increases the activity when the marker gene belongs to the group (b) , as compared to that in a control where the candidate compound has not been contacted,

wherein the marker gene is any one selected from the group according to (a) or (b) in claim 1, or a gene functionally equivalent to the marker gene.

23. A therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, which comprises as an active ingredient a compound being obtainable by any one of the screening methods according to claims 7, 20, 21, and 22.

24. A therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, which comprises as an active ingredient a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, or a polynucleotide that suppresses the expression of the gene through an RNAi effect, wherein the marker gene is any one selected from the group according to (a) in claim 1.

25. A therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, which comprises as an active ingredient an antibody recognizing a protein encoded by a marker gene, wherein the marker gene is any one selected from the group according to (a) in claim 1.

26. A therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, which comprises as an active ingredient a marker gene, or a protein encoded by a marker gene, wherein the marker gene is any one selected from the group according to (b) in claim 1.

27. A DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilized to assay a marker gene, and wherein the marker gene comprises at least a single type of gene selected from group (a) and (b) in claim 1.

DOCID: <EP_____1394274A2_I_>

Fig. 1

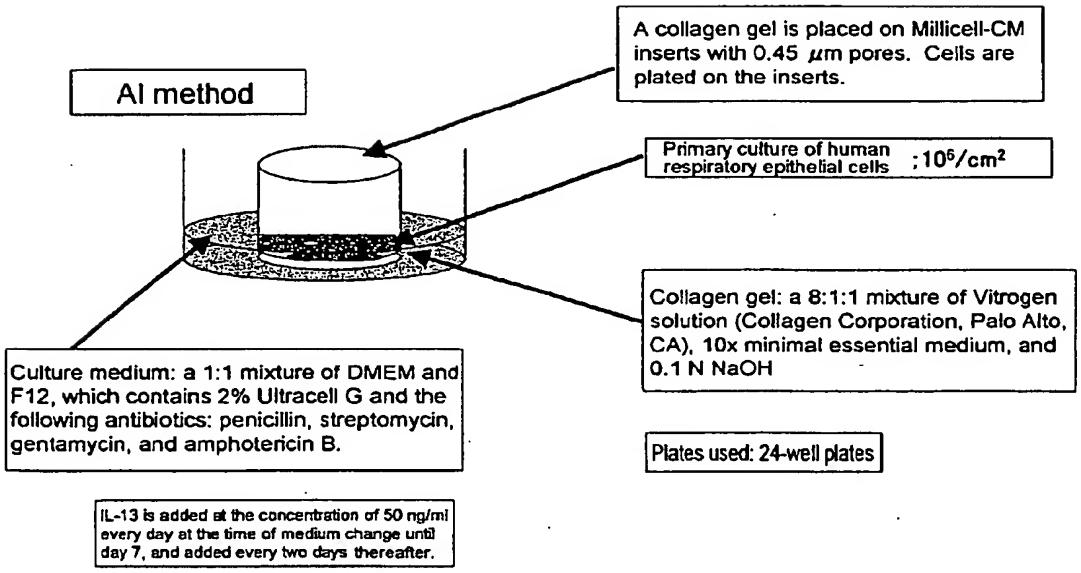


Fig. 2

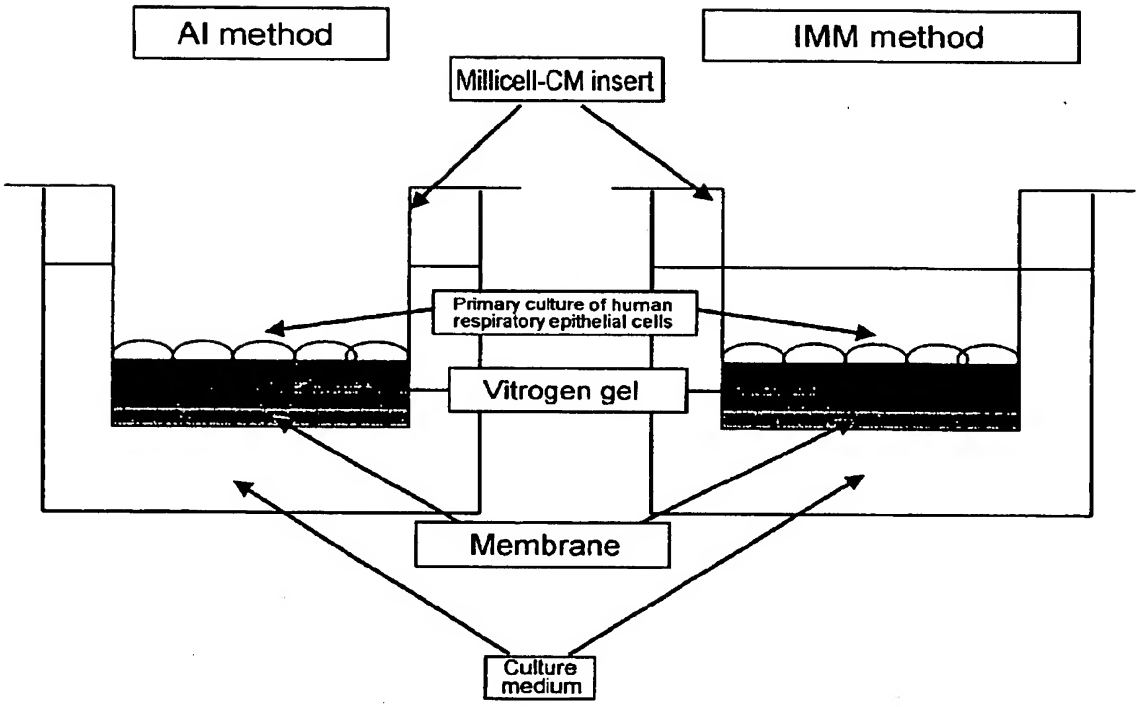


Fig. 3

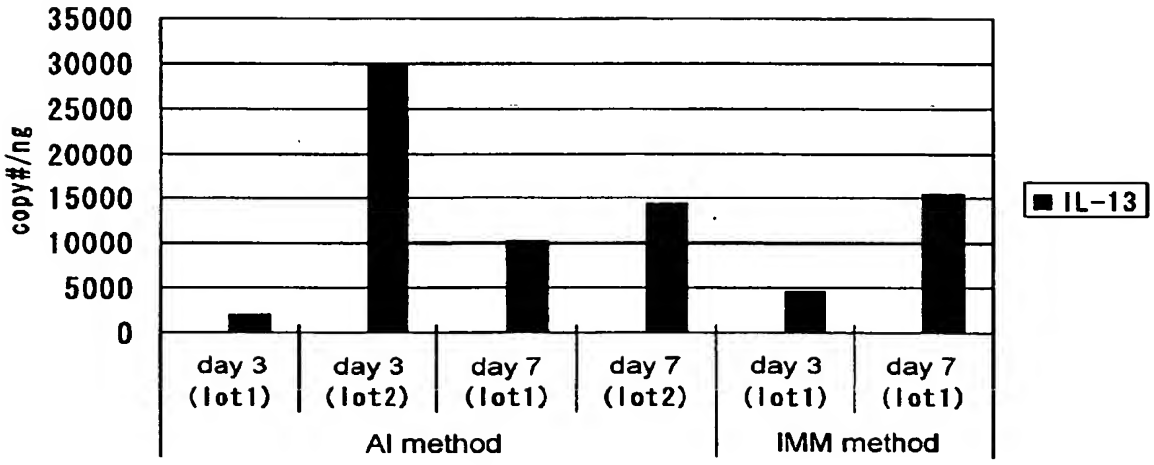


Fig. 4

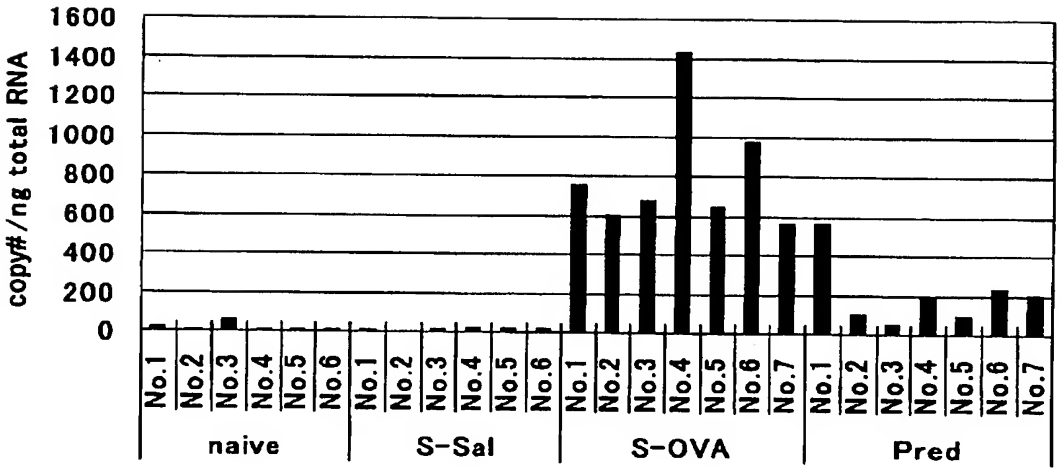


Fig. 5

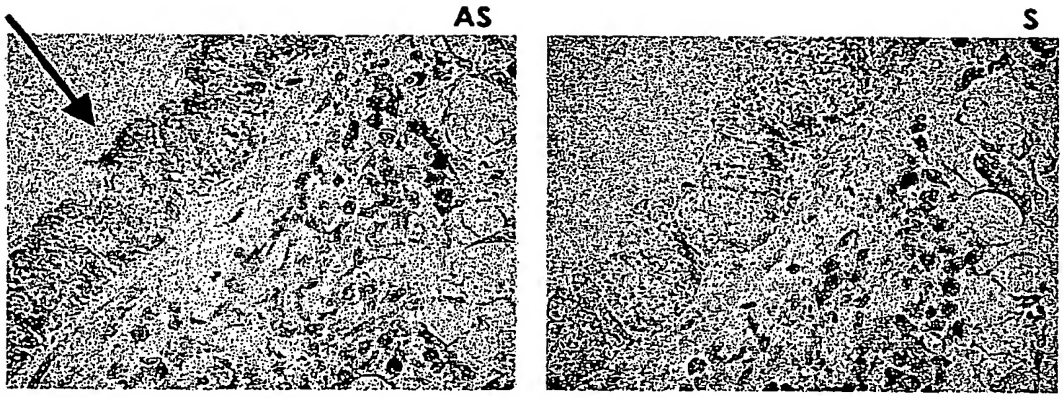


Fig. 6

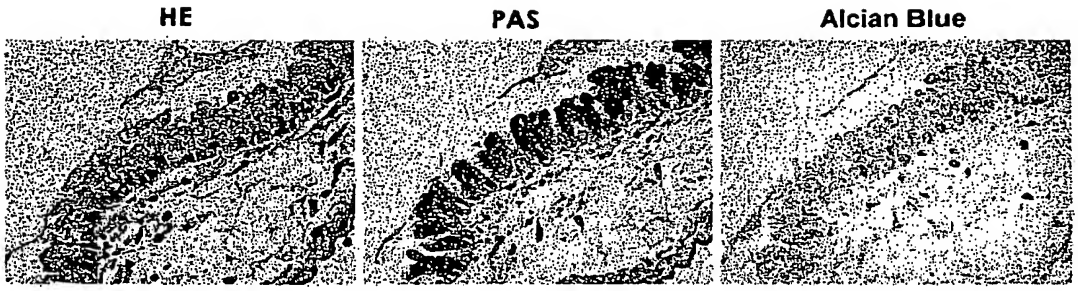
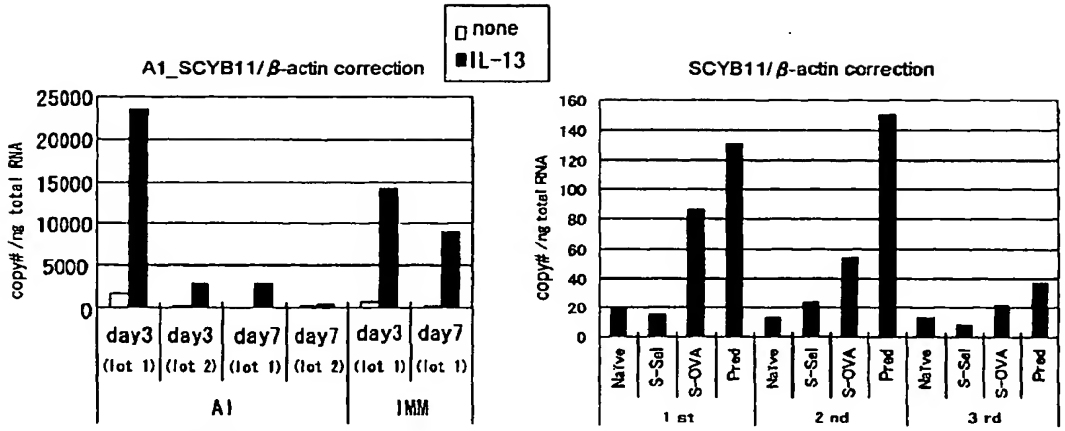


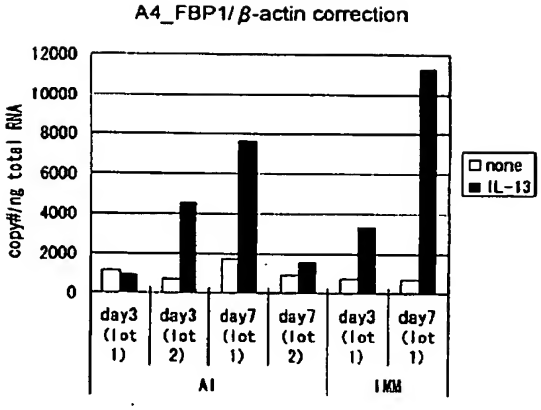
Fig. 7



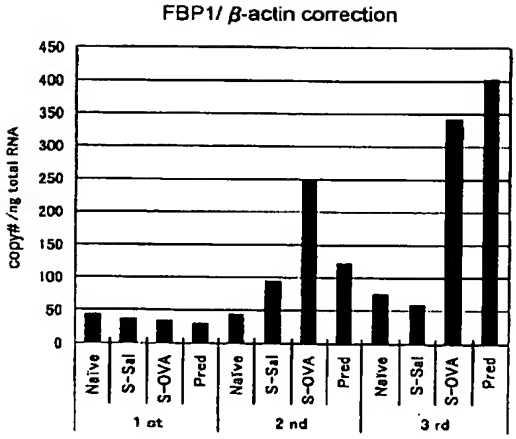
GOB panel increased

MASM5 panel increased

Fig. 8

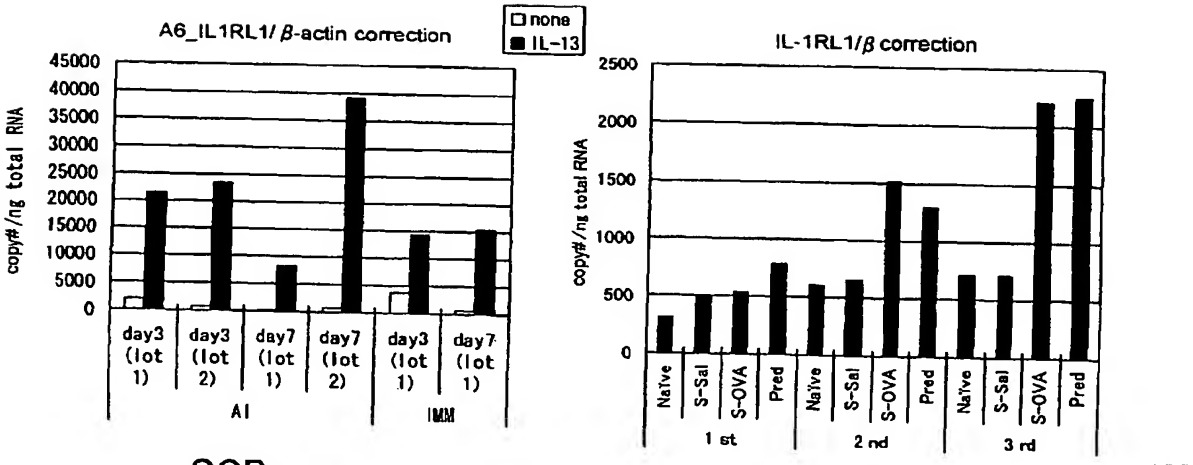


GOB panel increased



MASM5 panel increased

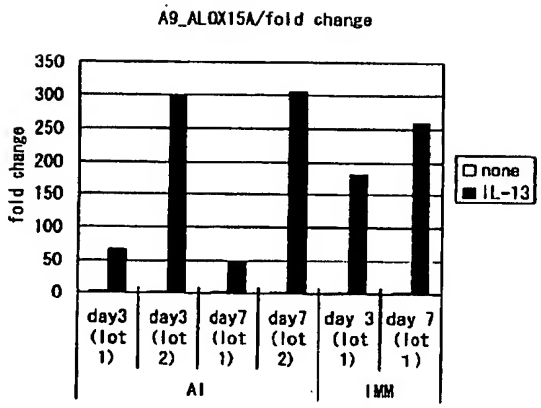
Fig. 9



GOB panel increased

MASM5 panel increased

Fig. 10



GOB panel
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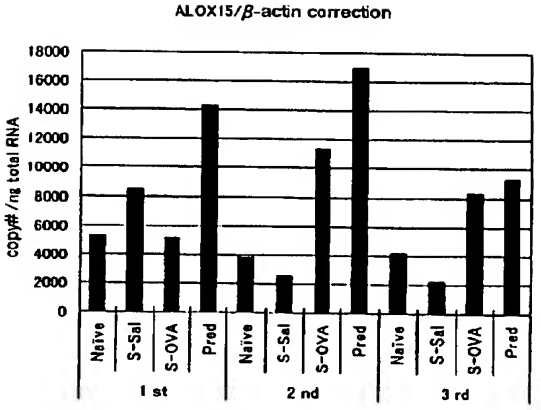
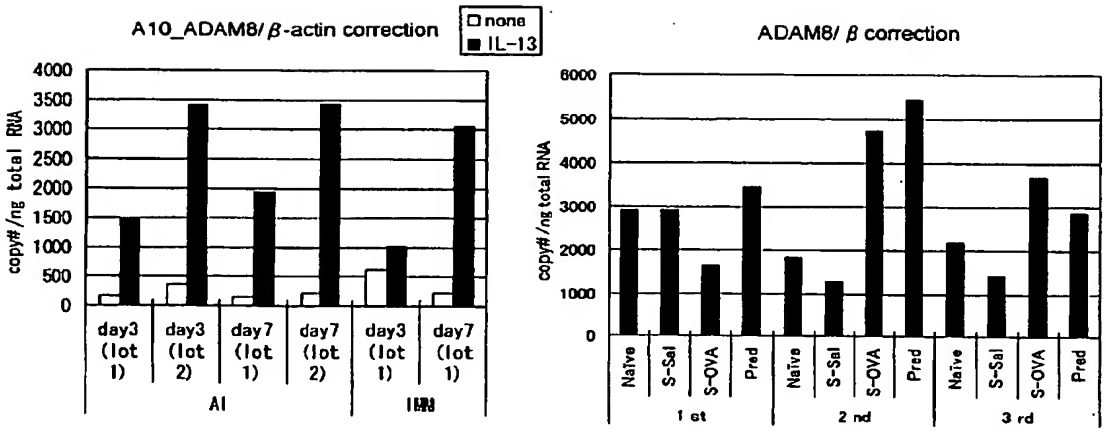


MASM5 panel
increased

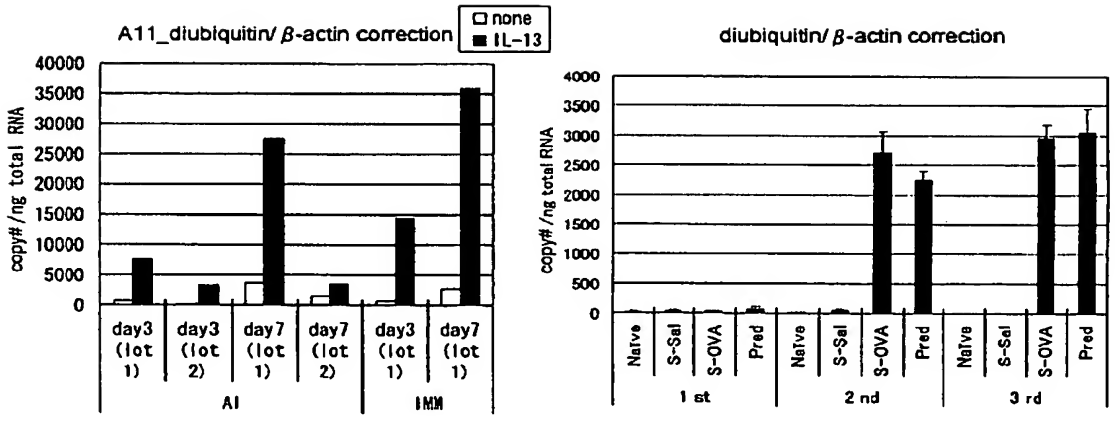
Fig. 11



GOB panel increased

MASM5 panel increased

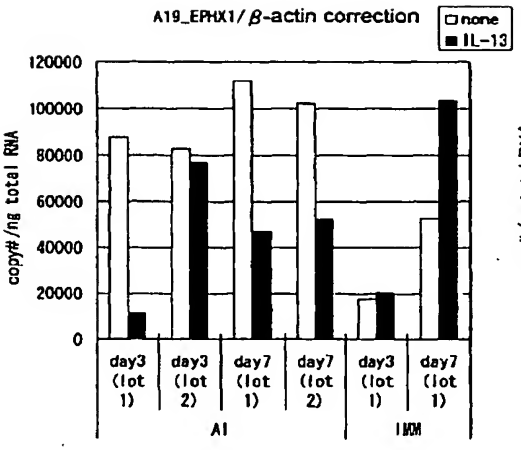
Fig. 12



GOB panel
increased

MASM5 panel
increasead

Fig. 13



GOB panel
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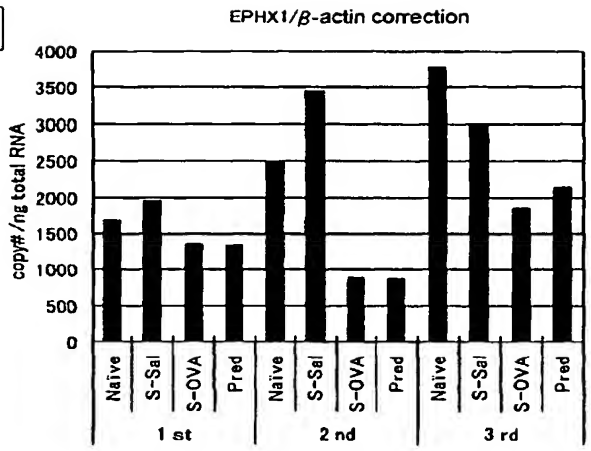
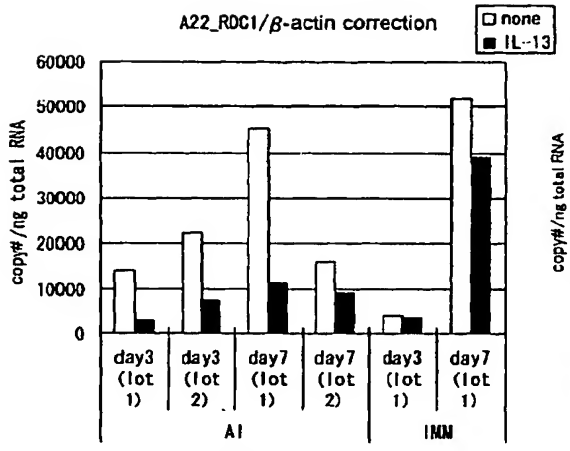
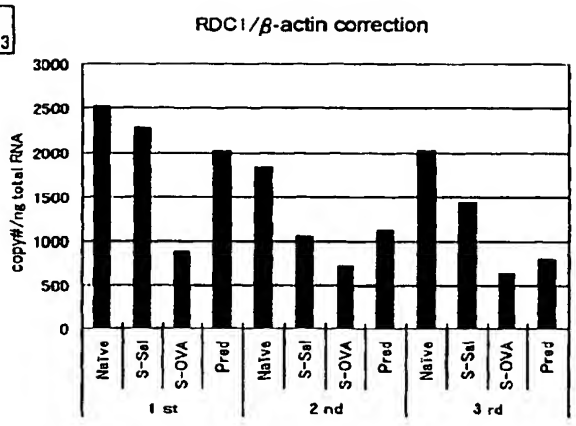


MASM5 panel
decreased

Fig. 14

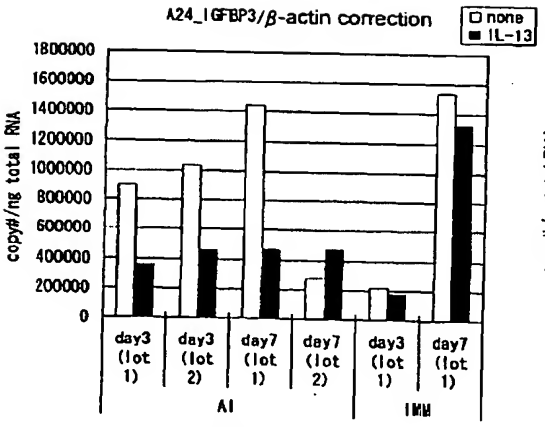


GOB panel
decreased

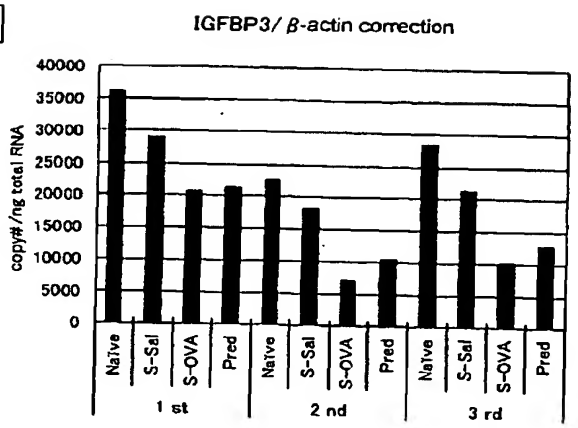


MASM5 panel
decreased

Fig. 15

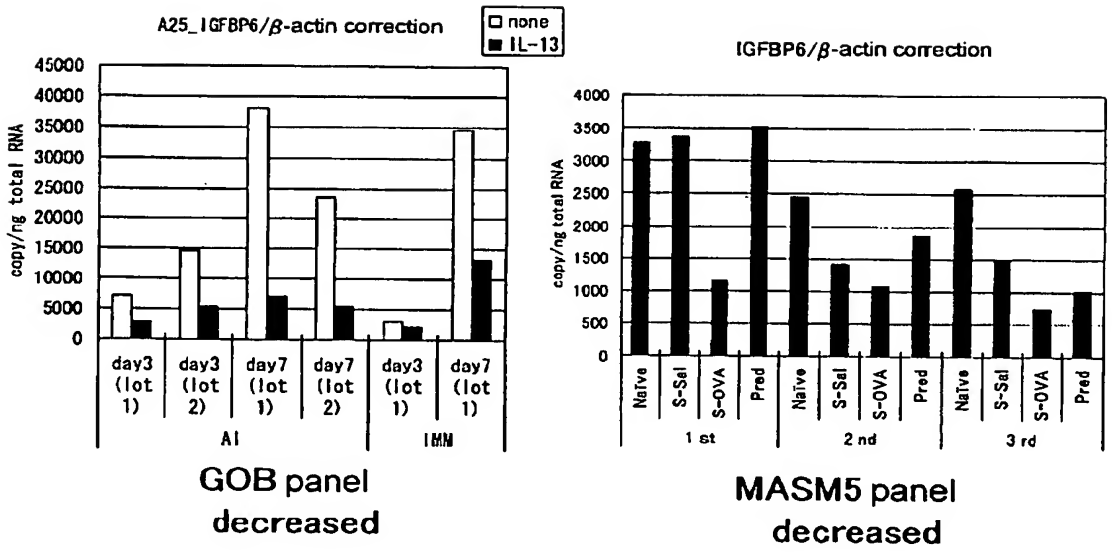


GOB panel
decreased



MASM5 panel
decreased

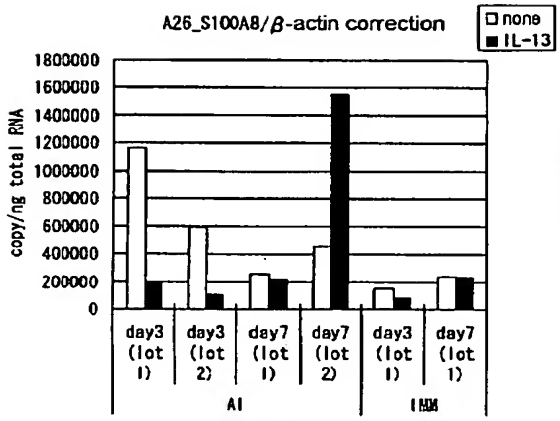
Fig. 16



GOB panel decreased

MASM5 panel decreased

Fig. 17



GOB panel
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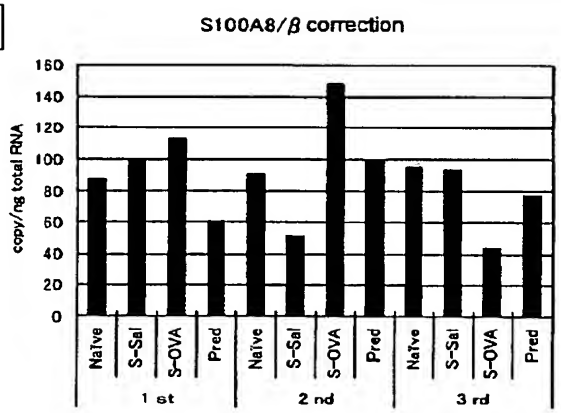

MASM5 panel
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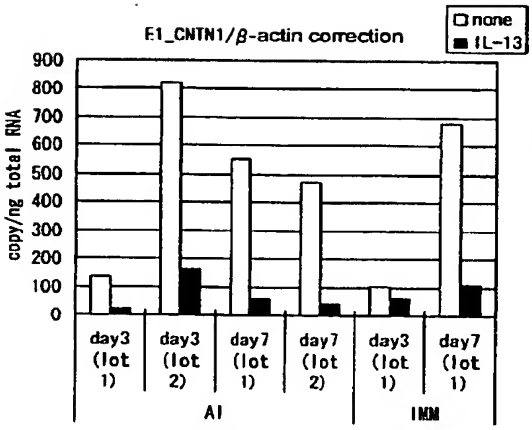
Fig. 18



GOB panel
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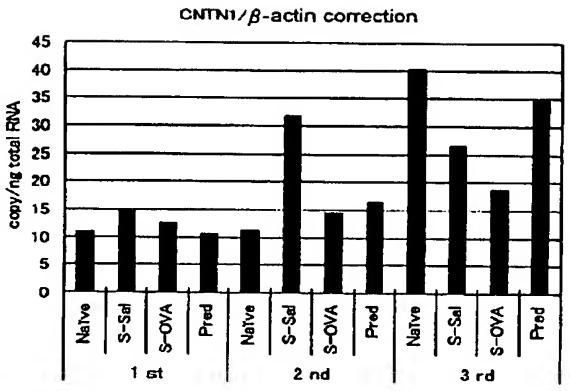
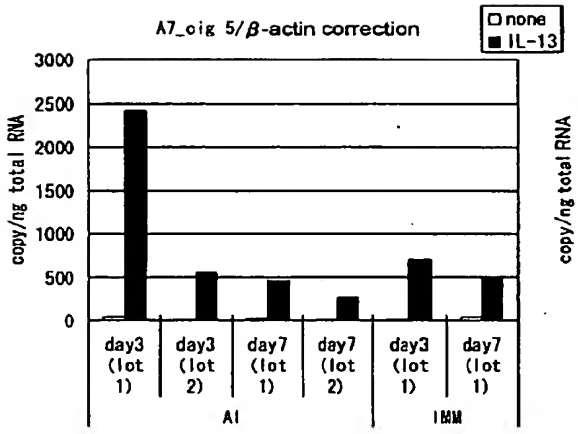
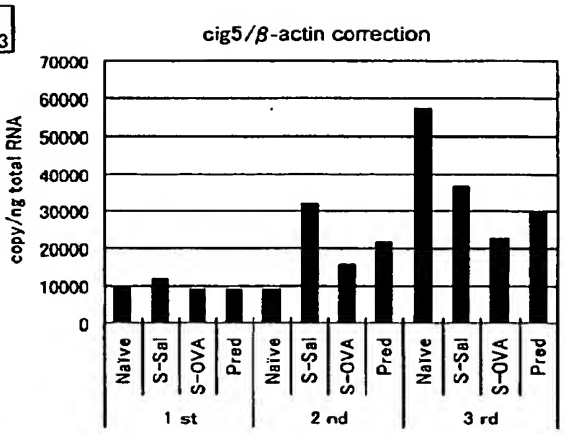


MASM5 panel-
decreased

Fig. 19



GOB panel
increased



MASM5 panel
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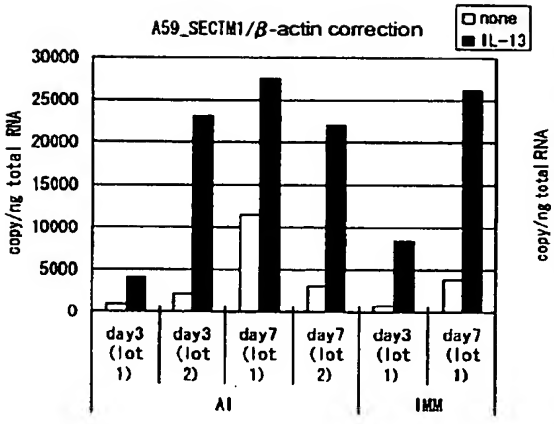
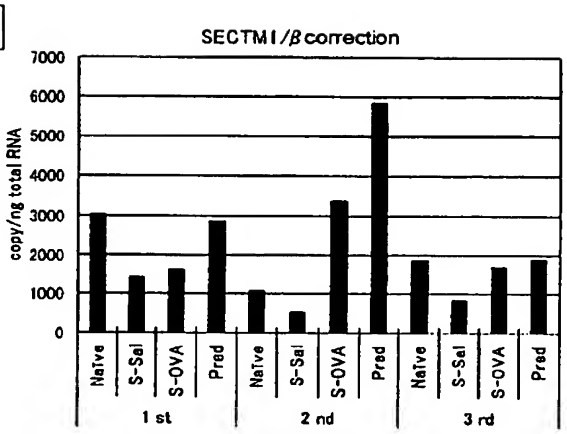
Fig. 20

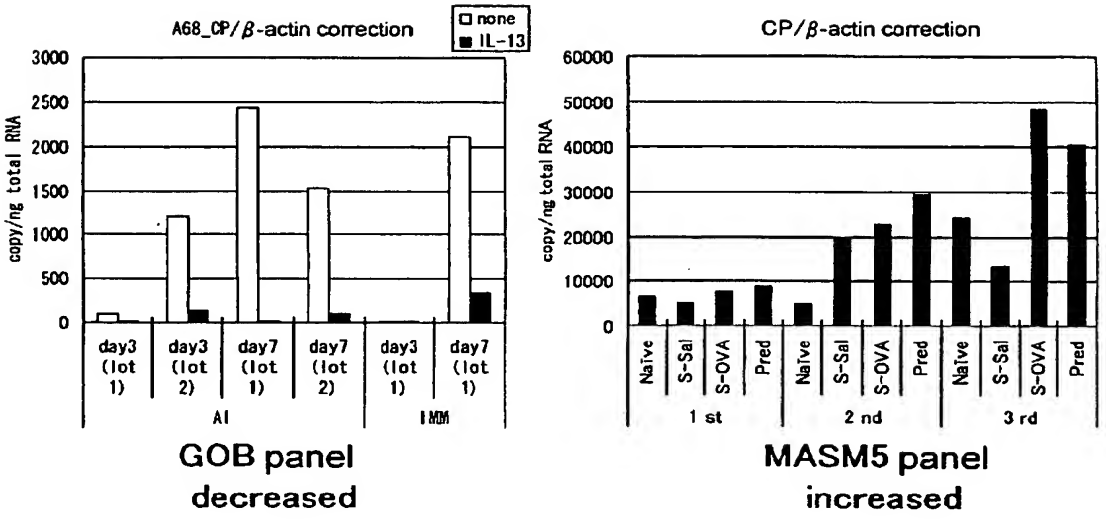


GOB panel
increased



MASM5 panel
decreased

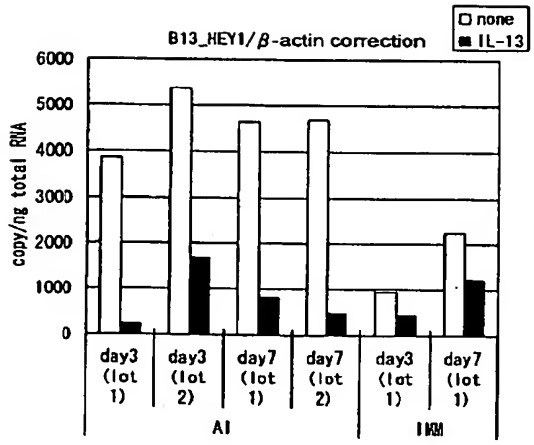
Fig. 21



GOB panel
decreased

MASM5 panel
increased

Fig. 22



GOB panel
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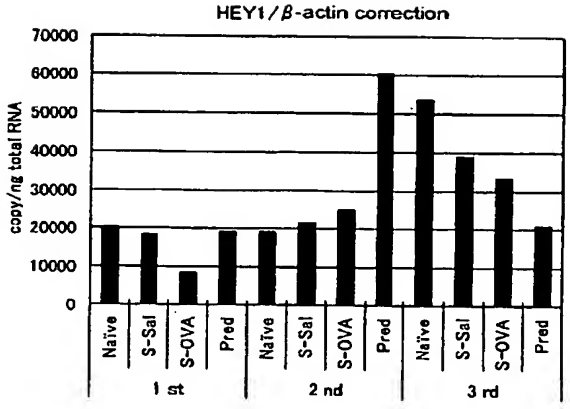
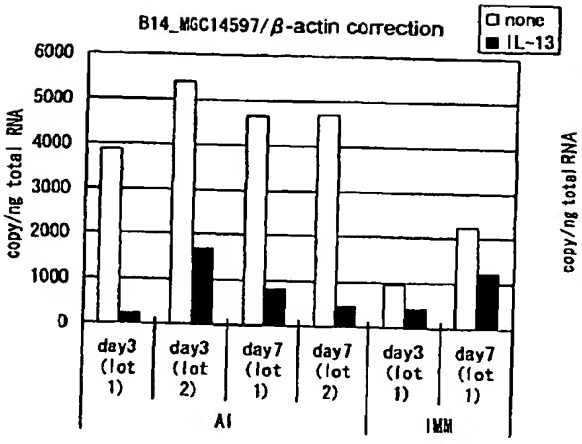


MASM5 panel
increased

Fig. 23



GOB panel
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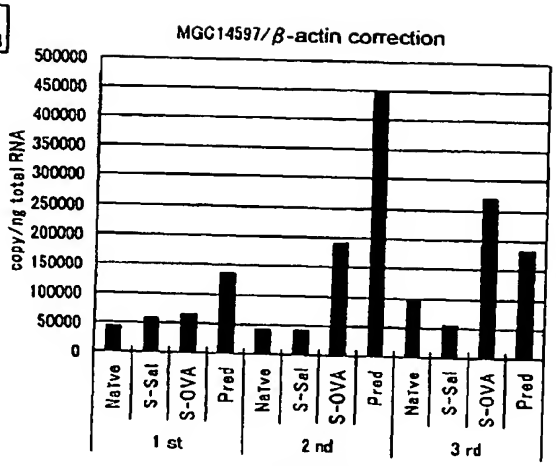
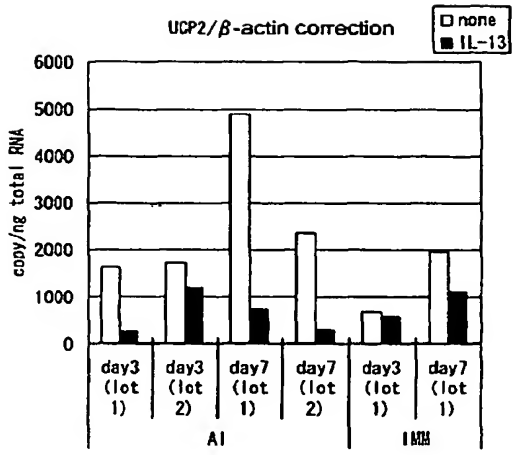
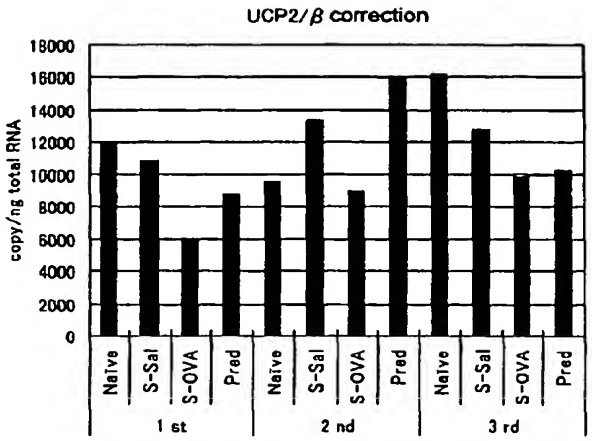


MASM5 panel
increased

Fig. 24



GOB panel
decreased



MASM5 panel
decreased

Fig. 25

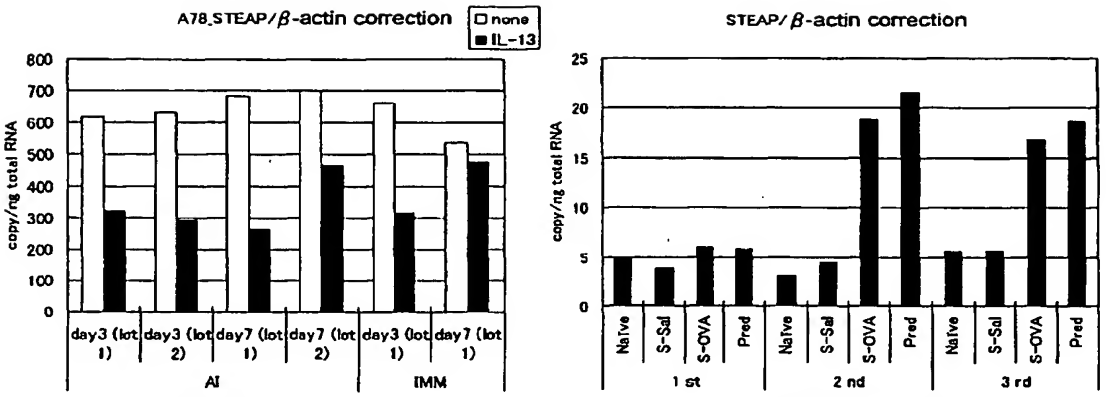


Fig. 26

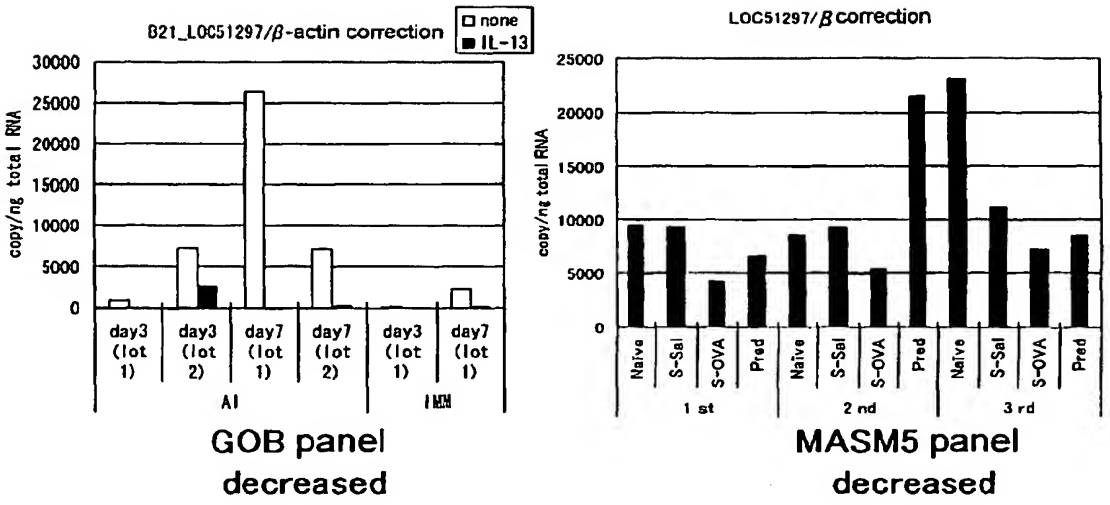
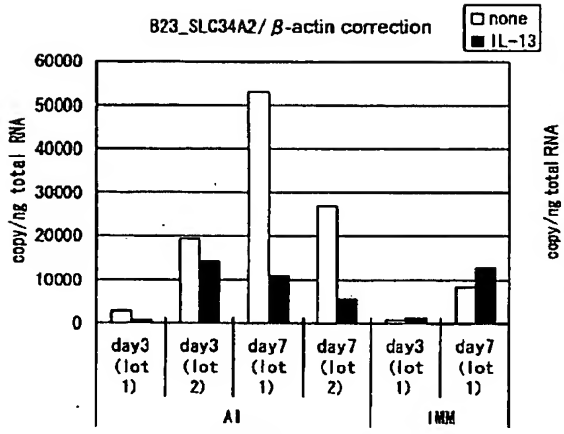
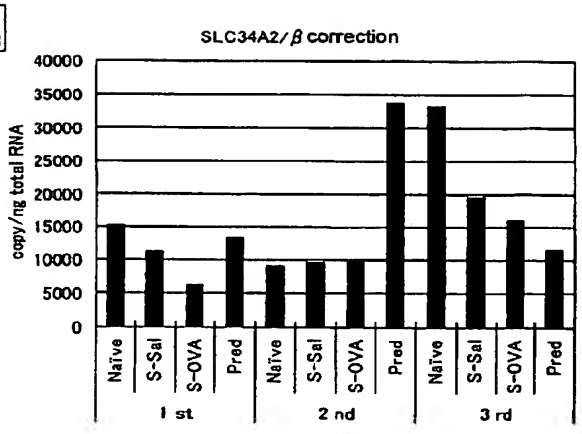


Fig. 27

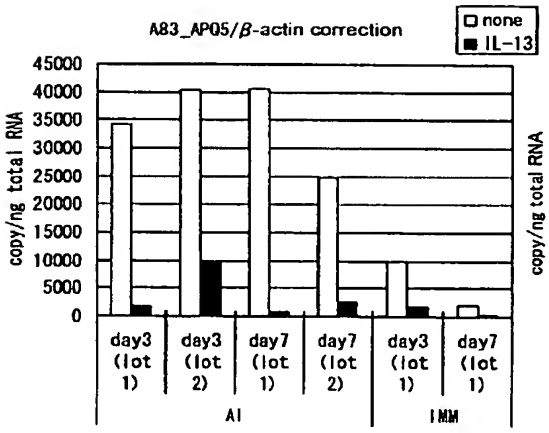


GOB panel
decreased

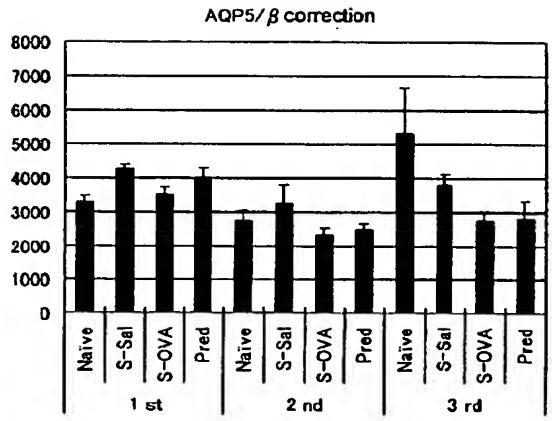


MASM5 panel
decreased

Fig. 28



GOB panel decreased



MASM5 panel decreased

Fig. 29

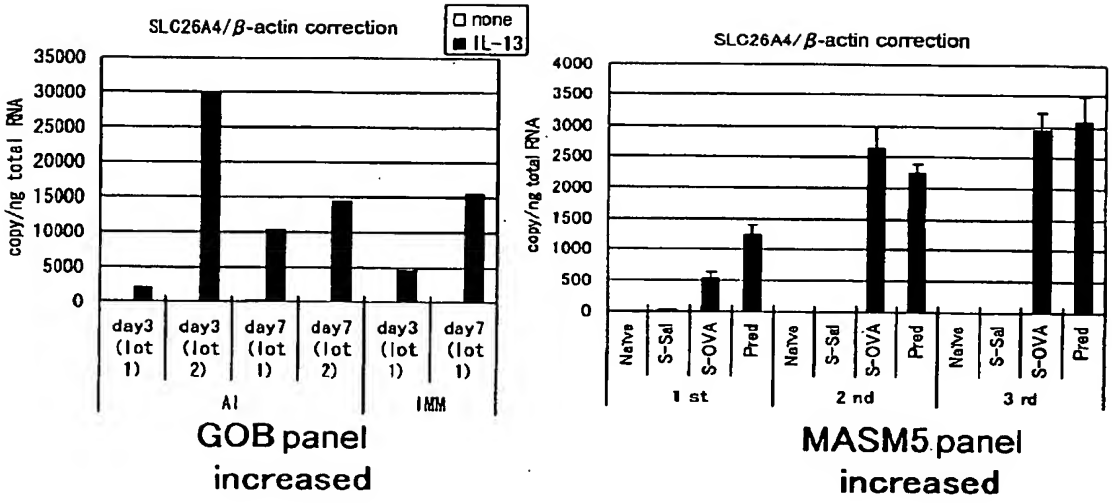
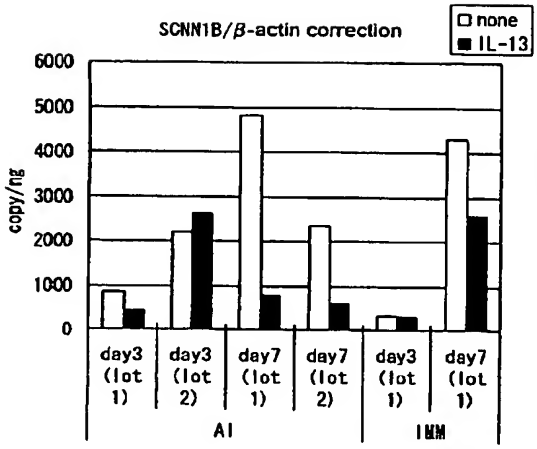
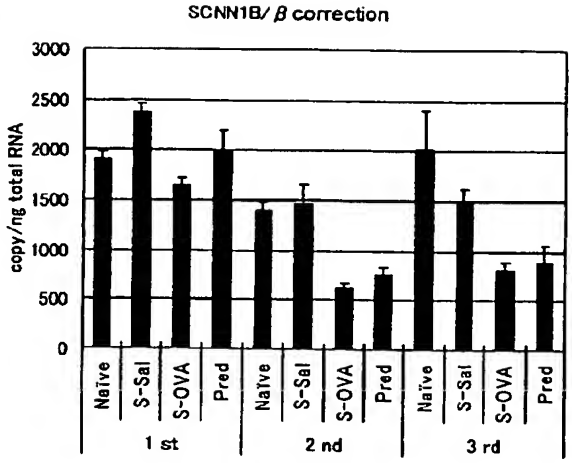


Fig. 30



GOB panel
decreased



MASM5 panel
decreased

Fig. 31

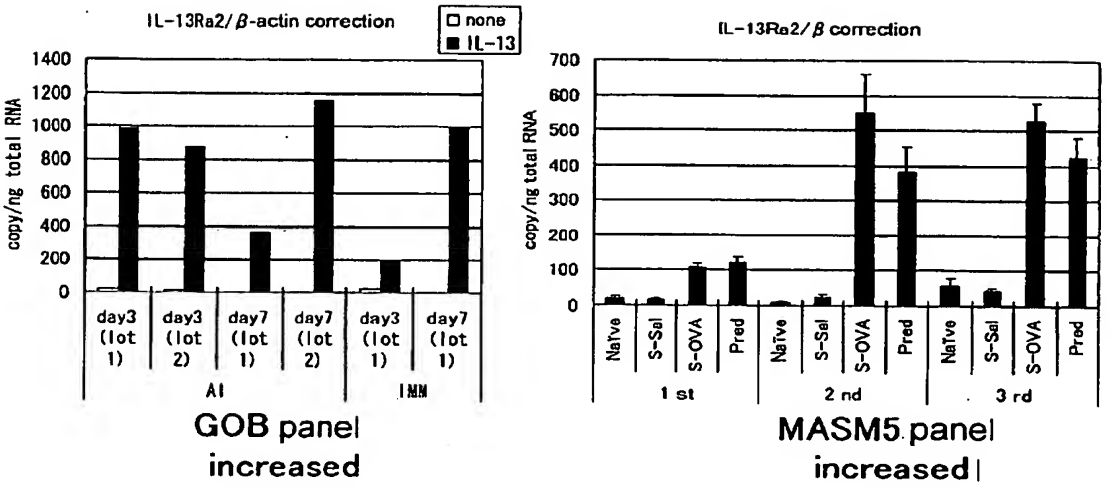
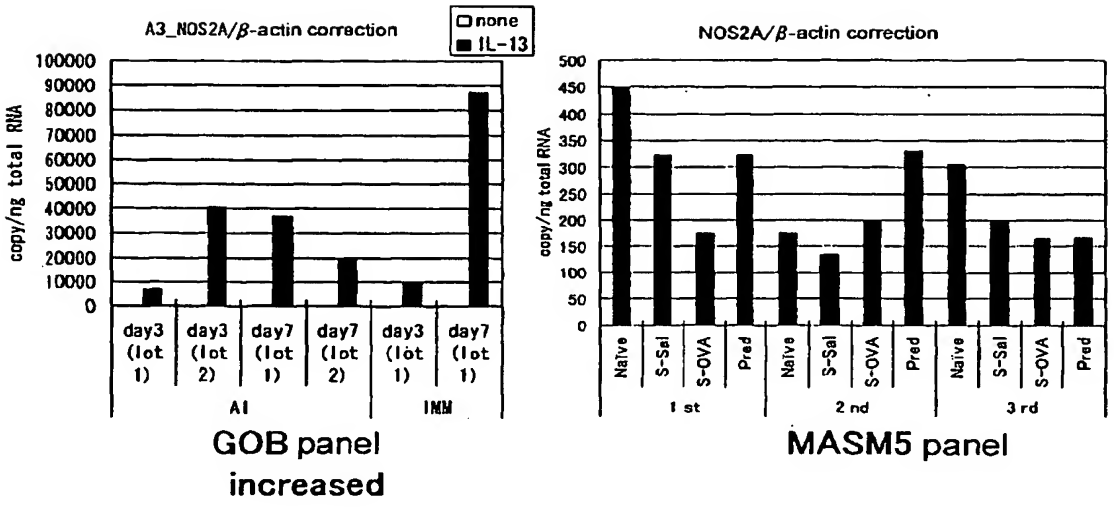


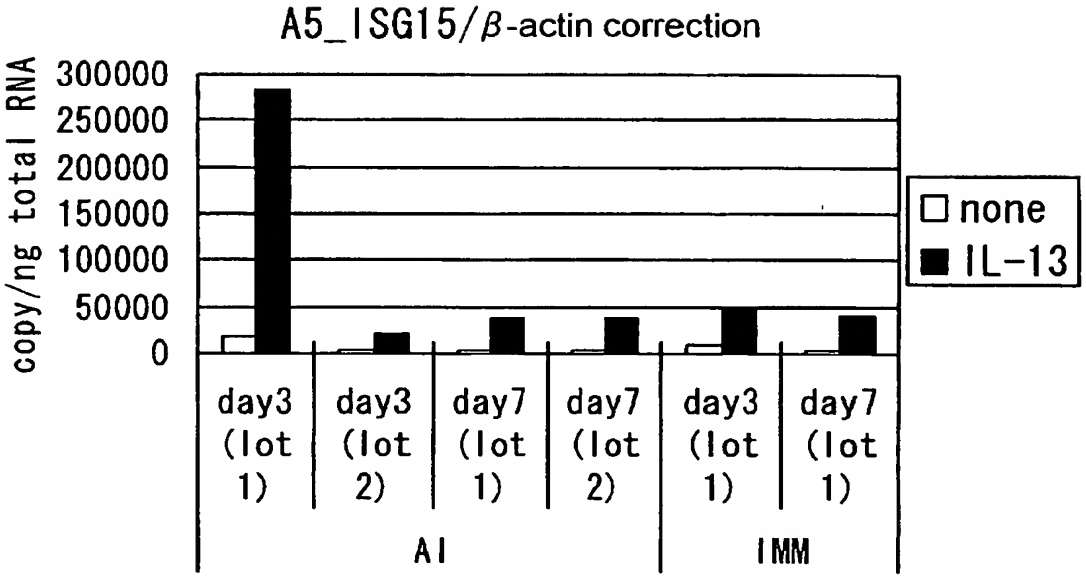
Fig. 32



GOB panel increased

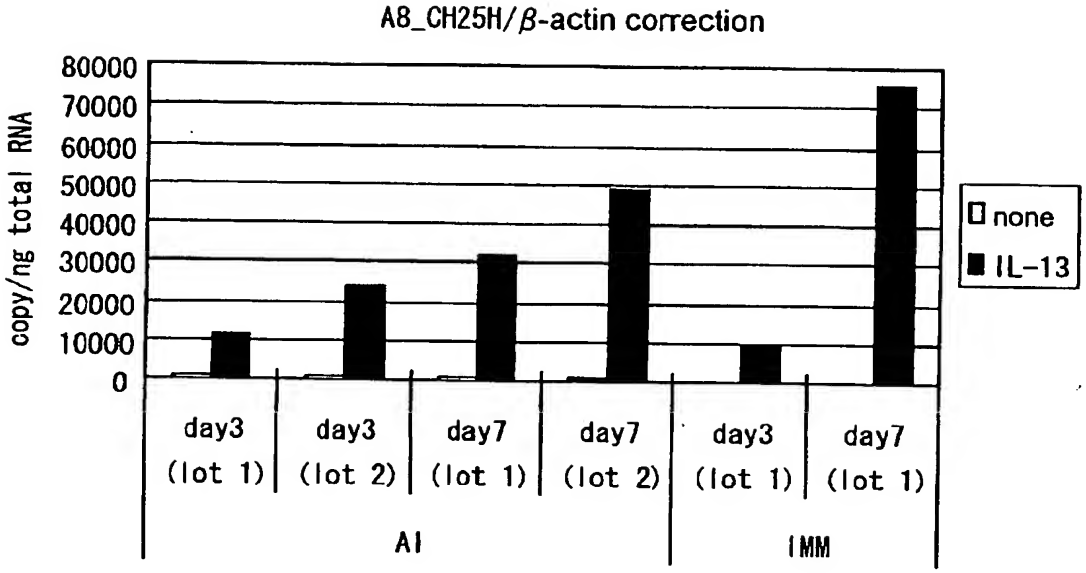
MASM5 panel

Fig. 33



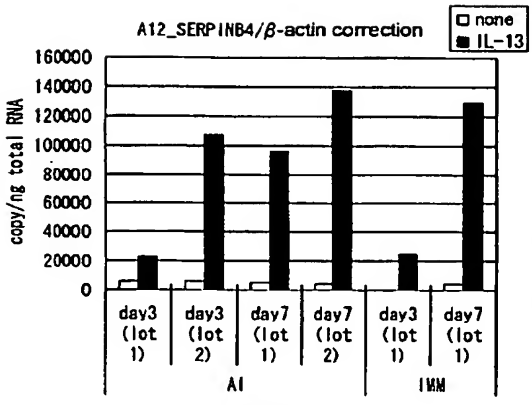
GOB panel
increased

Fig. 34

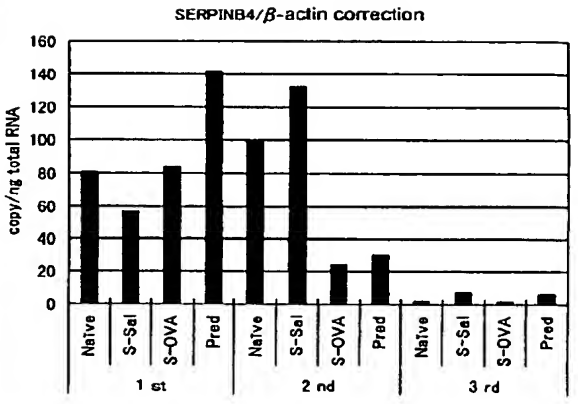


GOB panel increased

Fig. 35

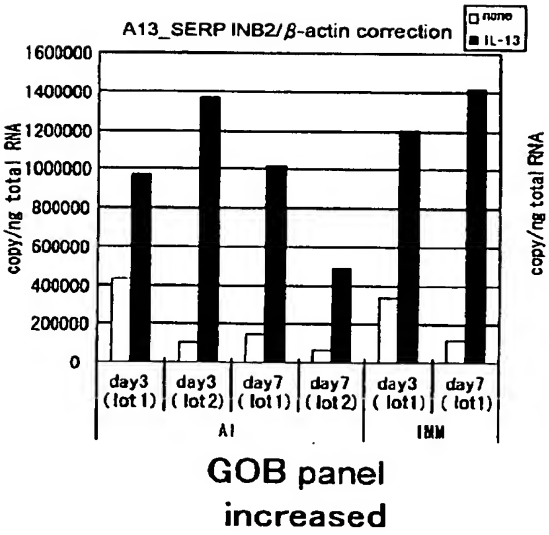


GOB panel
increased

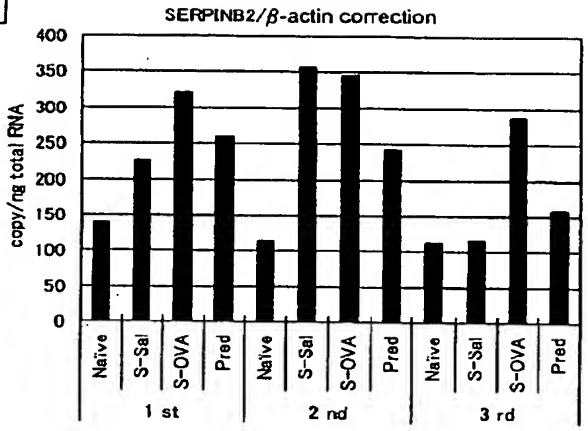


MASM5 panel

Fig. 36



GOB panel
increased



MASM5 panel

Fig. 37

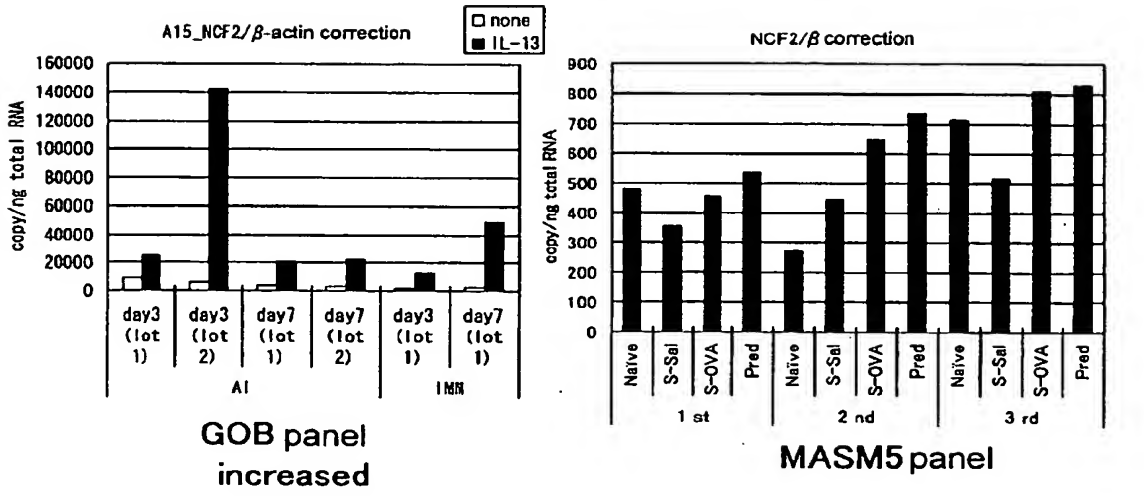


Fig. 38

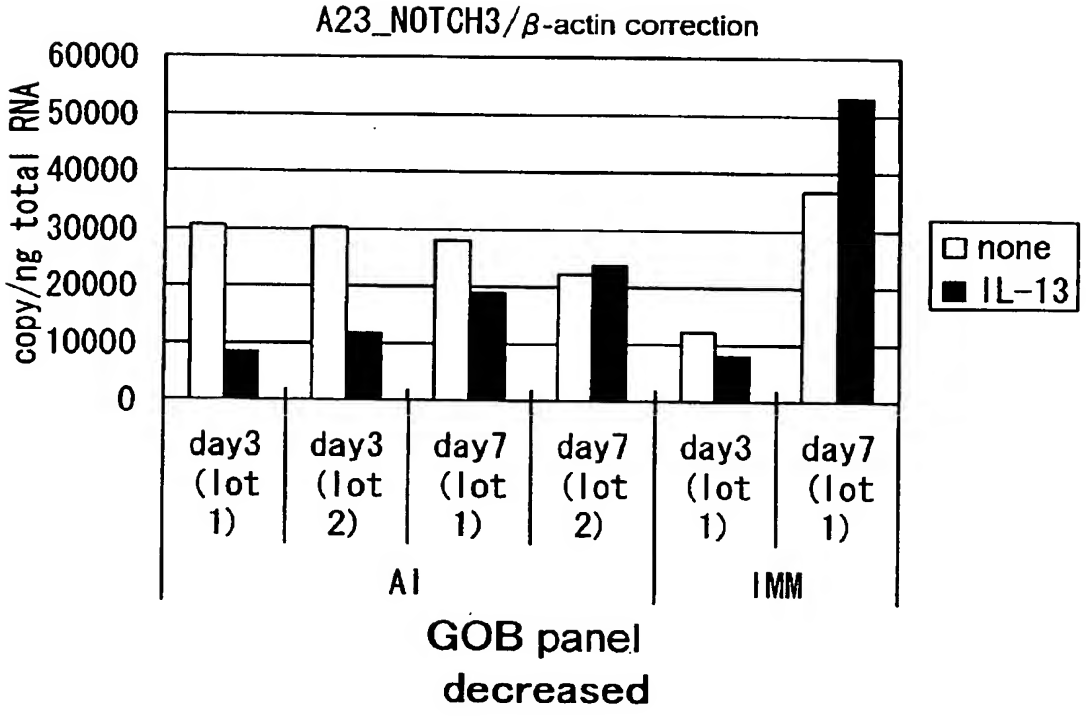


Fig. 39

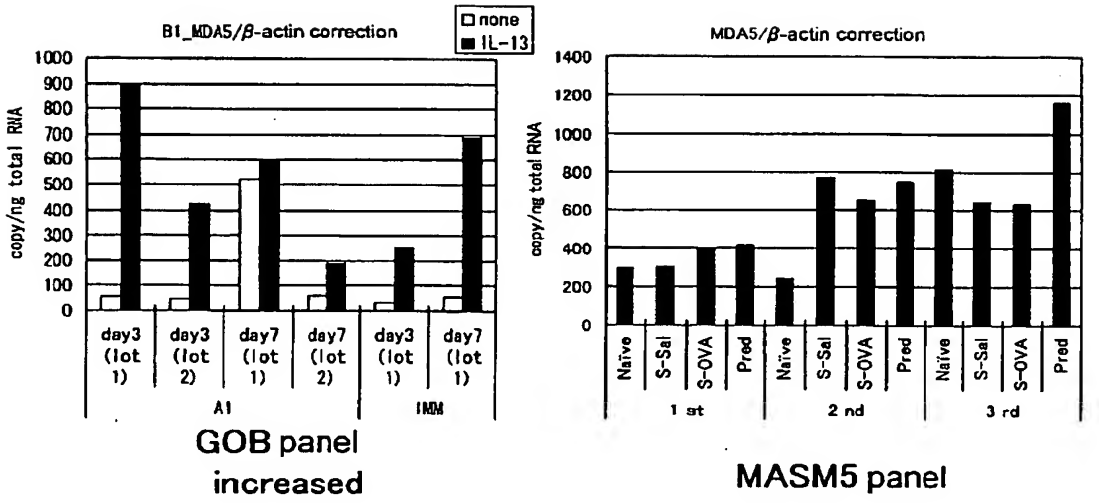


Fig. 40

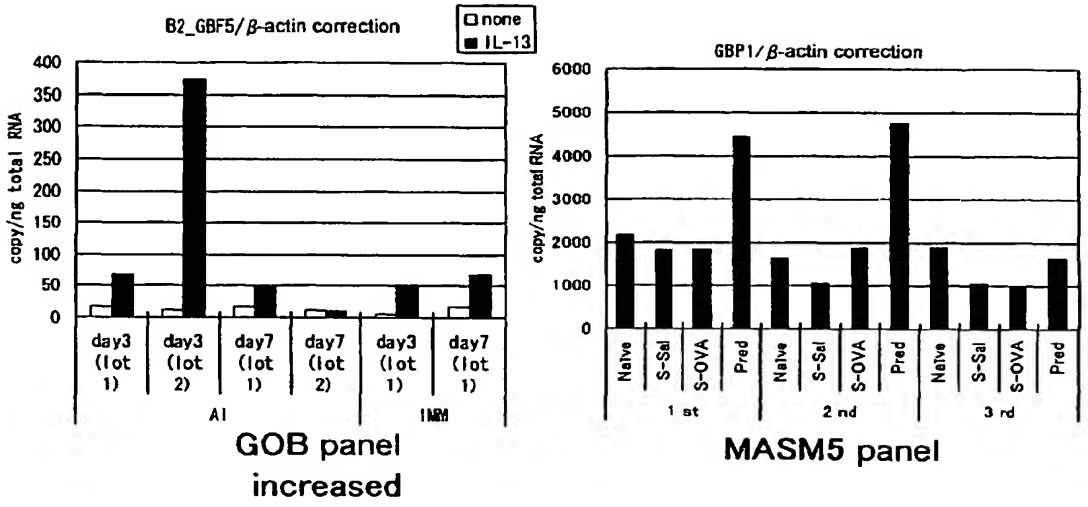


Fig. 41

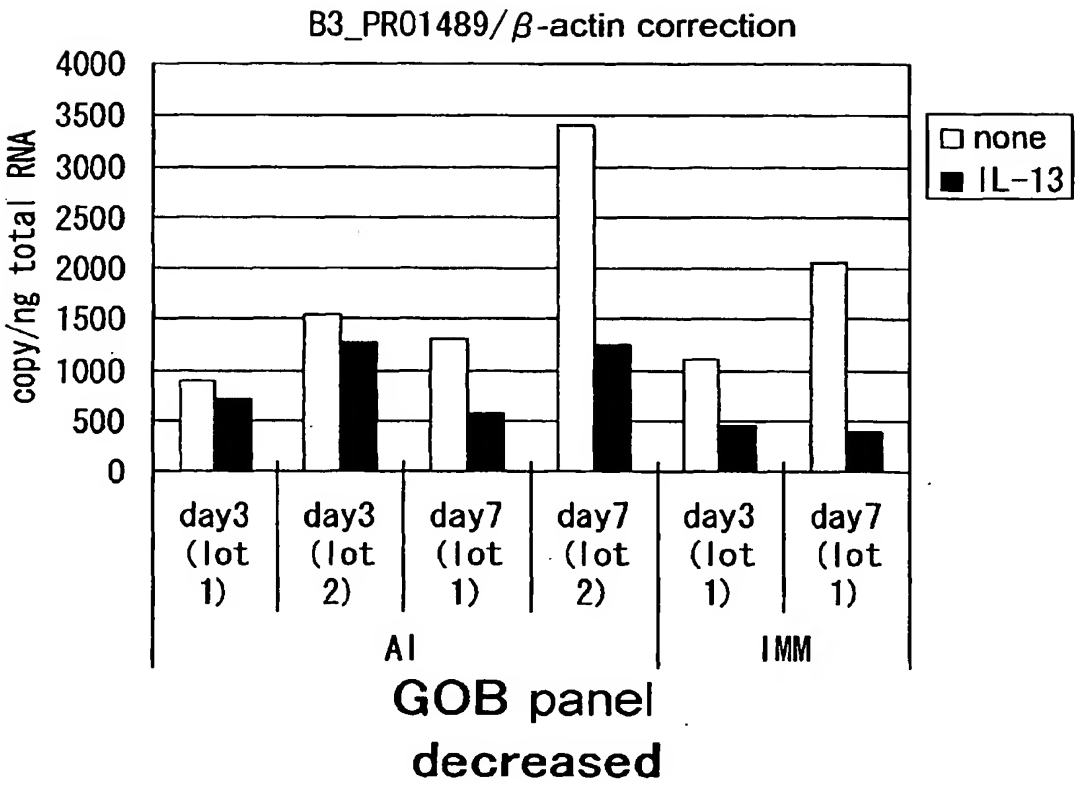
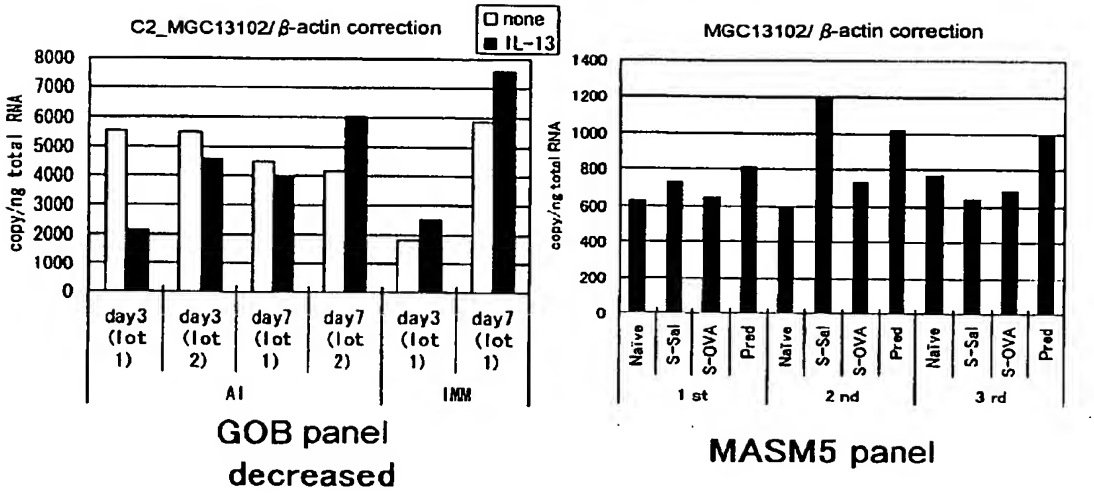


Fig. 42



GOB panel decreased

MASM5 panel

Fig. 43

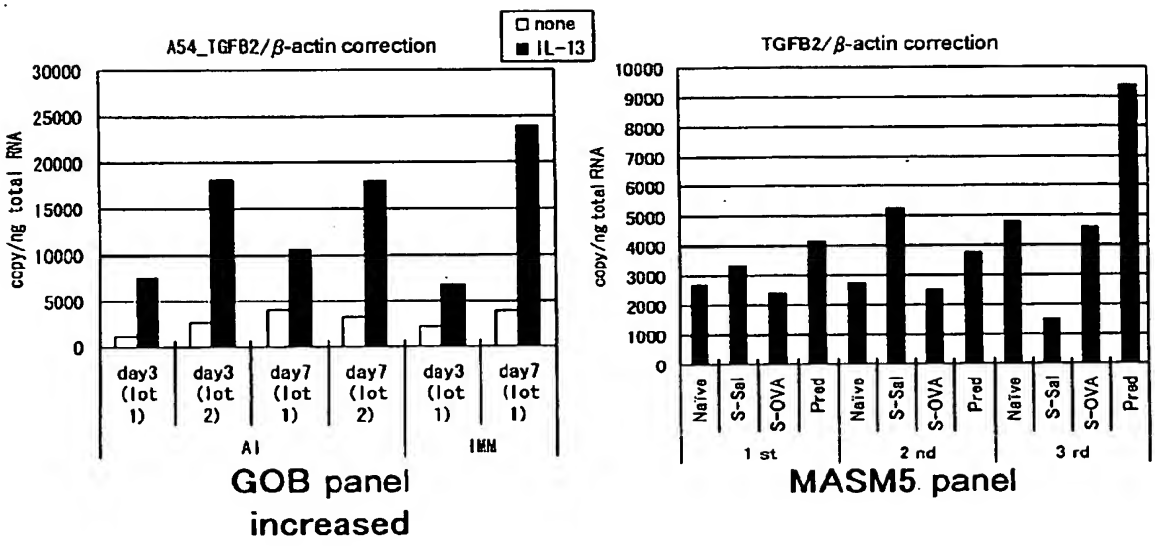


Fig. 44

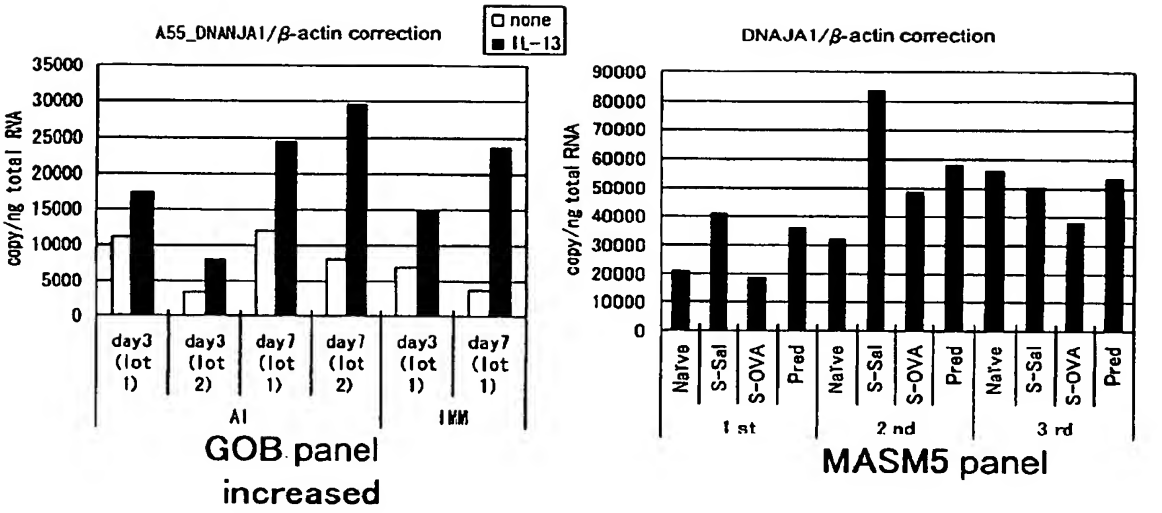


Fig. 45

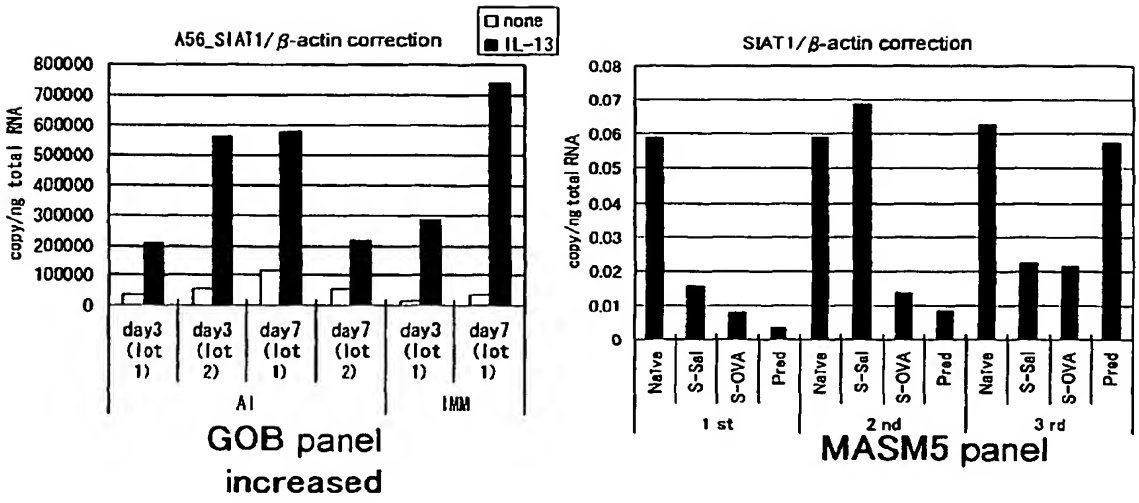


Fig. 46

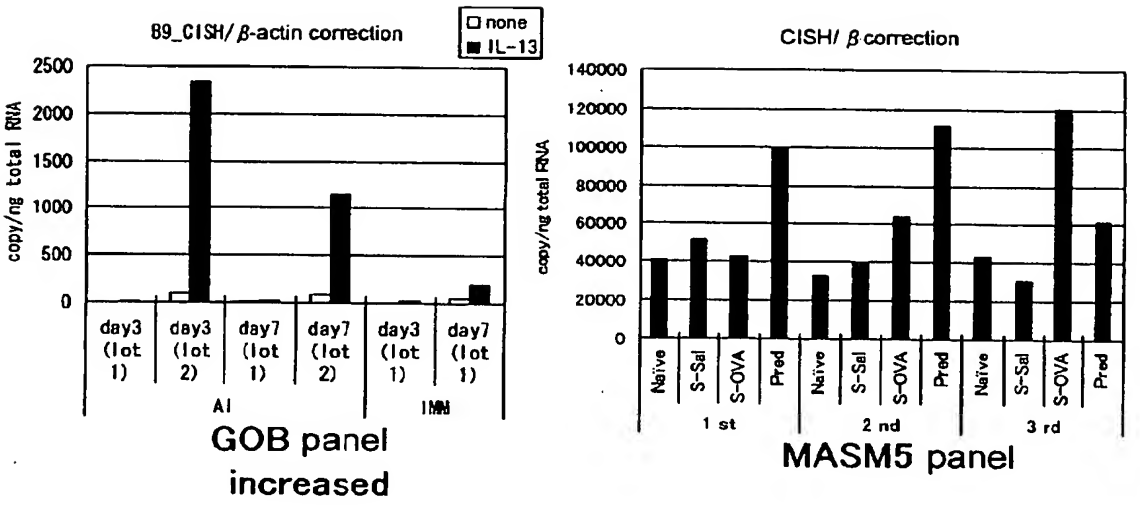


Fig. 47

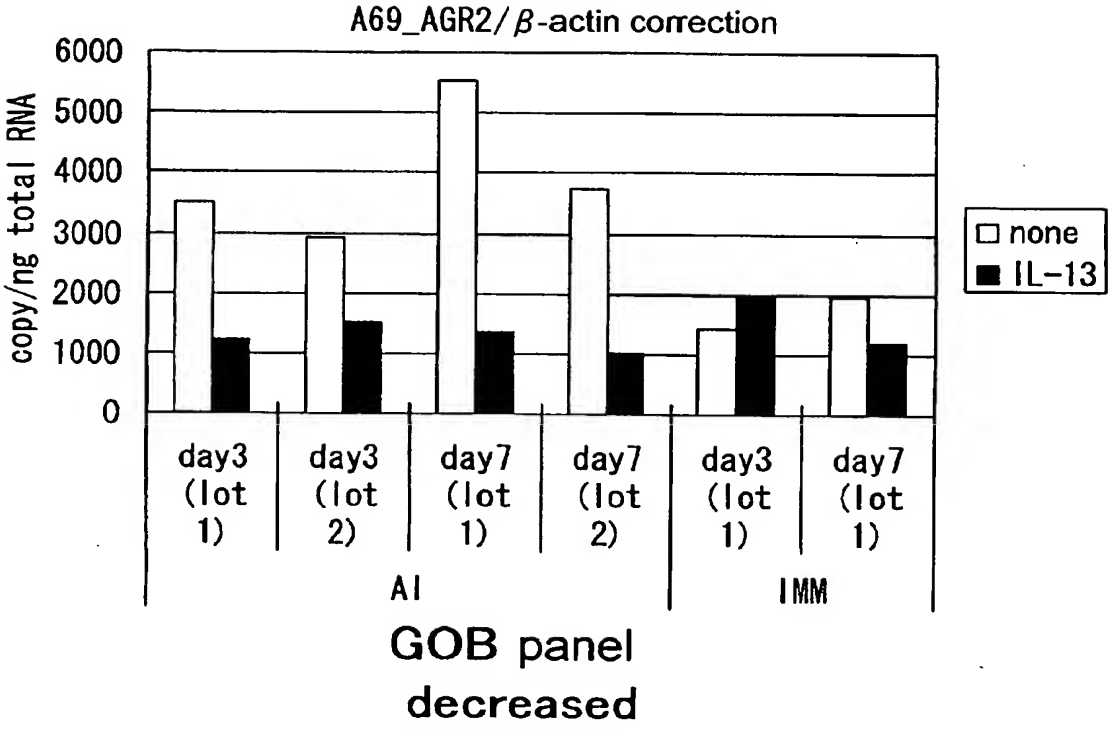
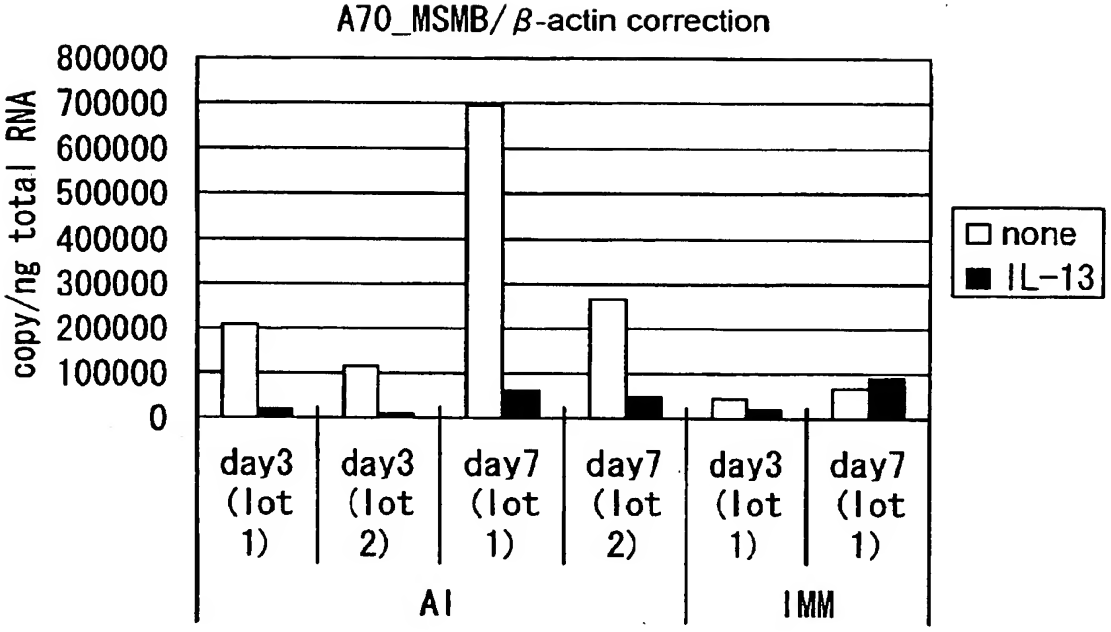


Fig. 48



GOB panel
decreased

Fig. 49

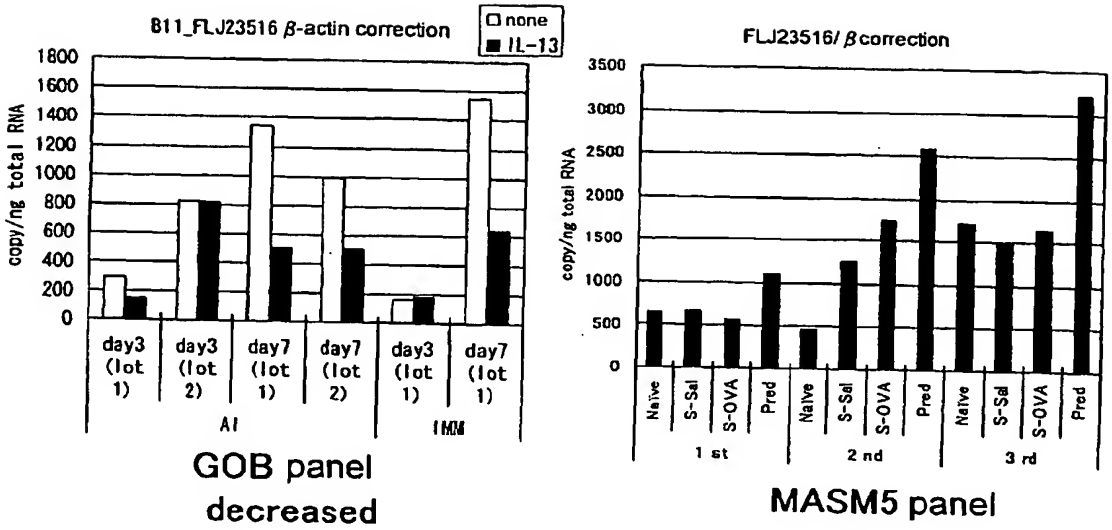
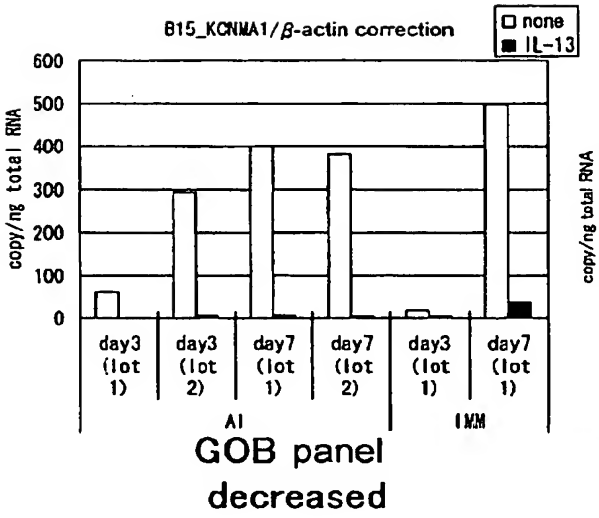
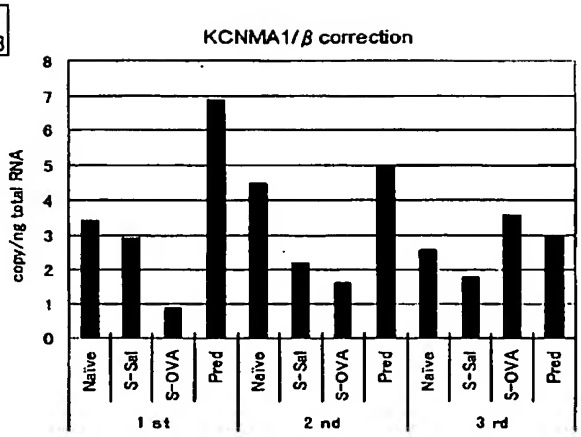


Fig. 50

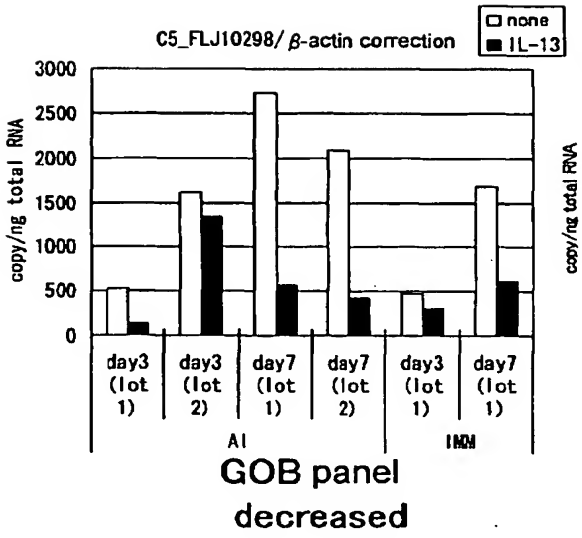


GOB panel
decreased

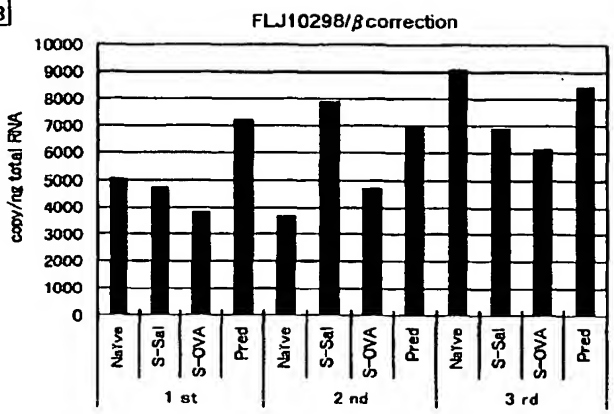


MASM5 panel

Fig. 51



GOB panel
decreased



MASM5 panel

Fig. 52

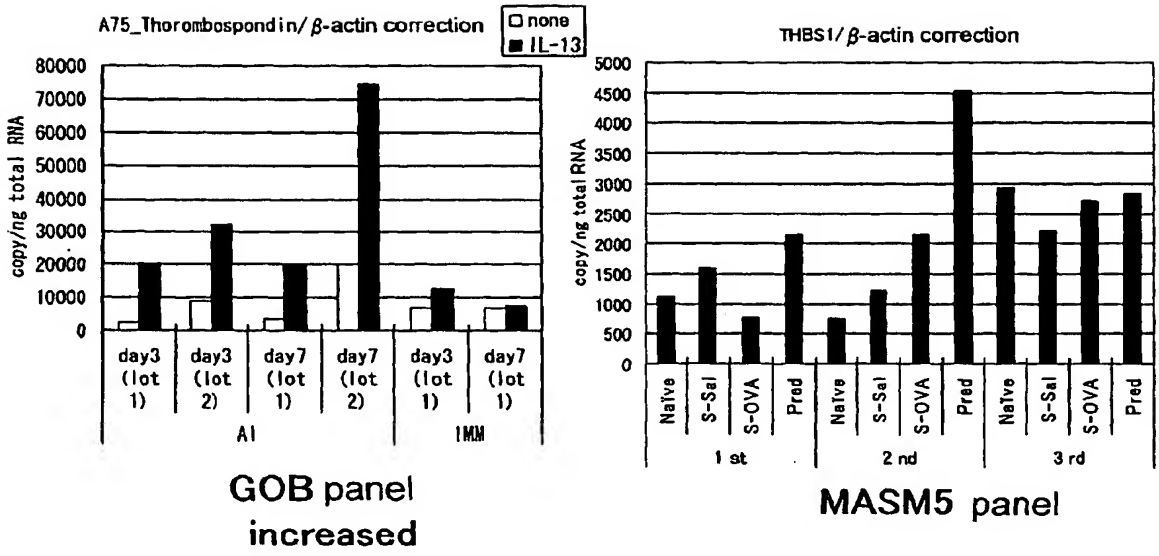
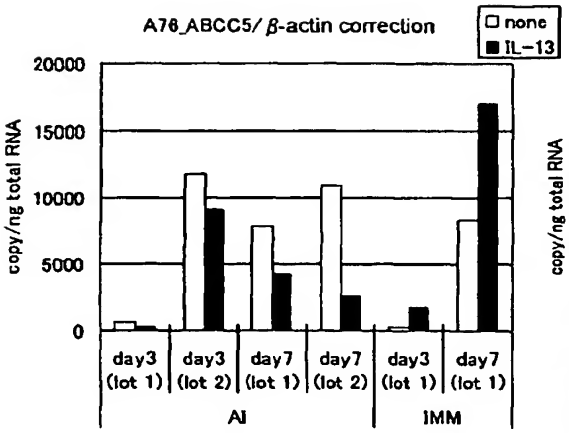
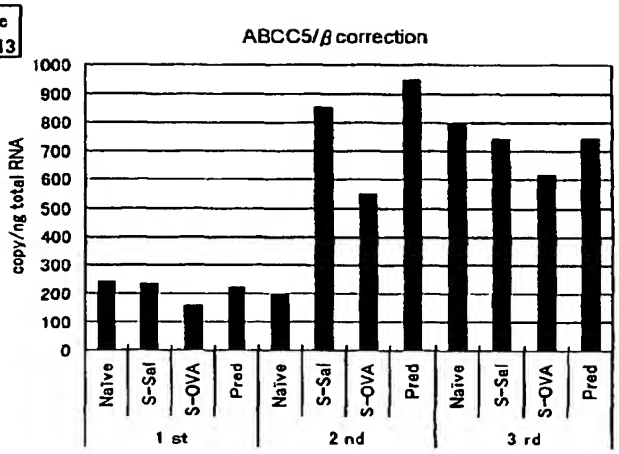


Fig. 53

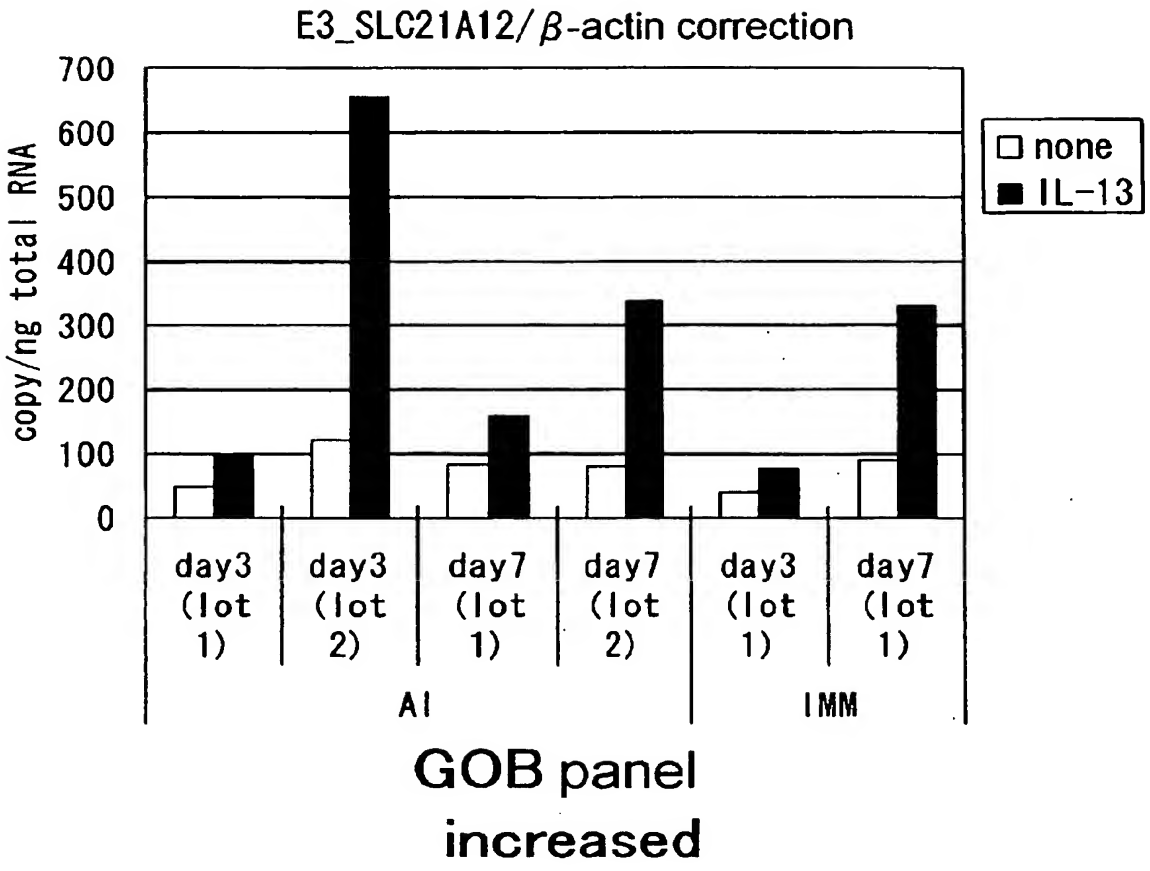


GOB panel
decreased



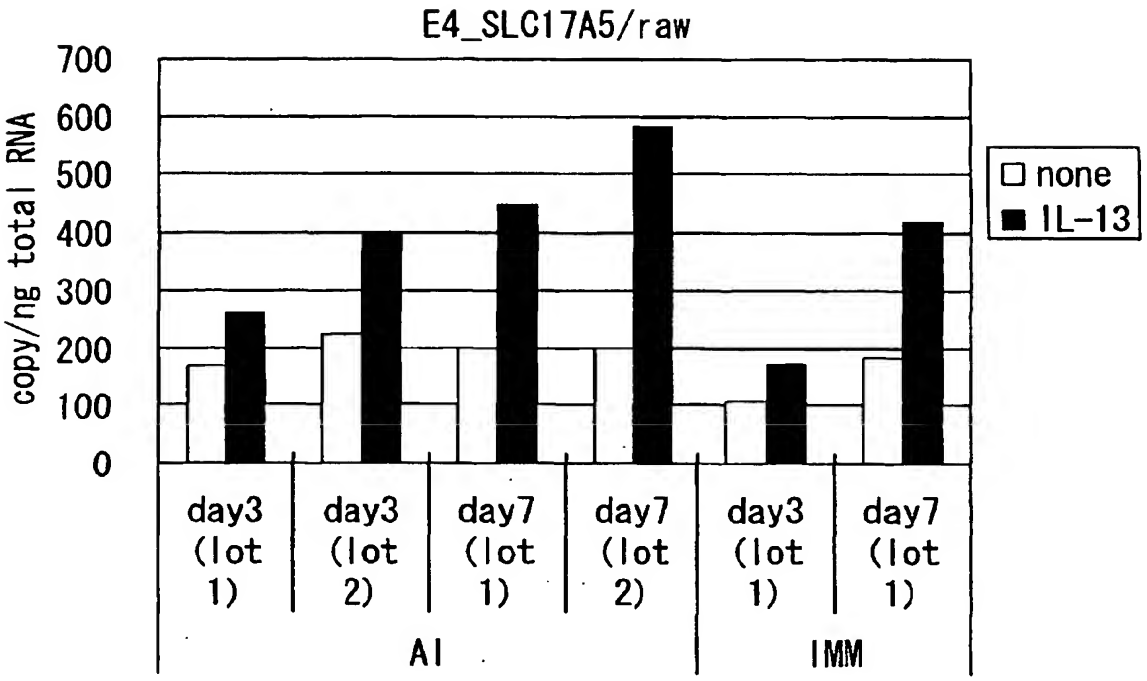
MASM5 panel

Fig. 54



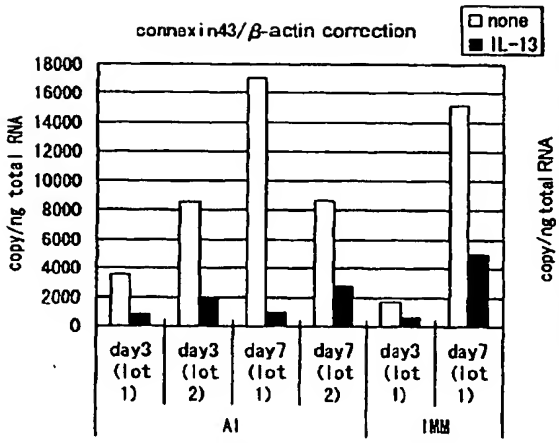
GOB panel increased

Fig. 55

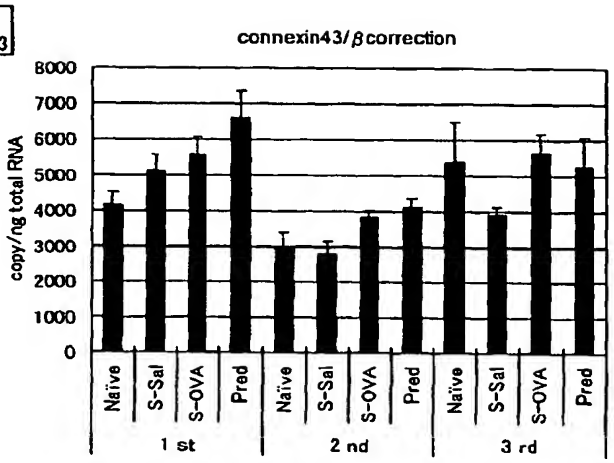


GOB panel increased

Fig. 56



GOB panel
decreased



MASM5 panel

Fig. 57

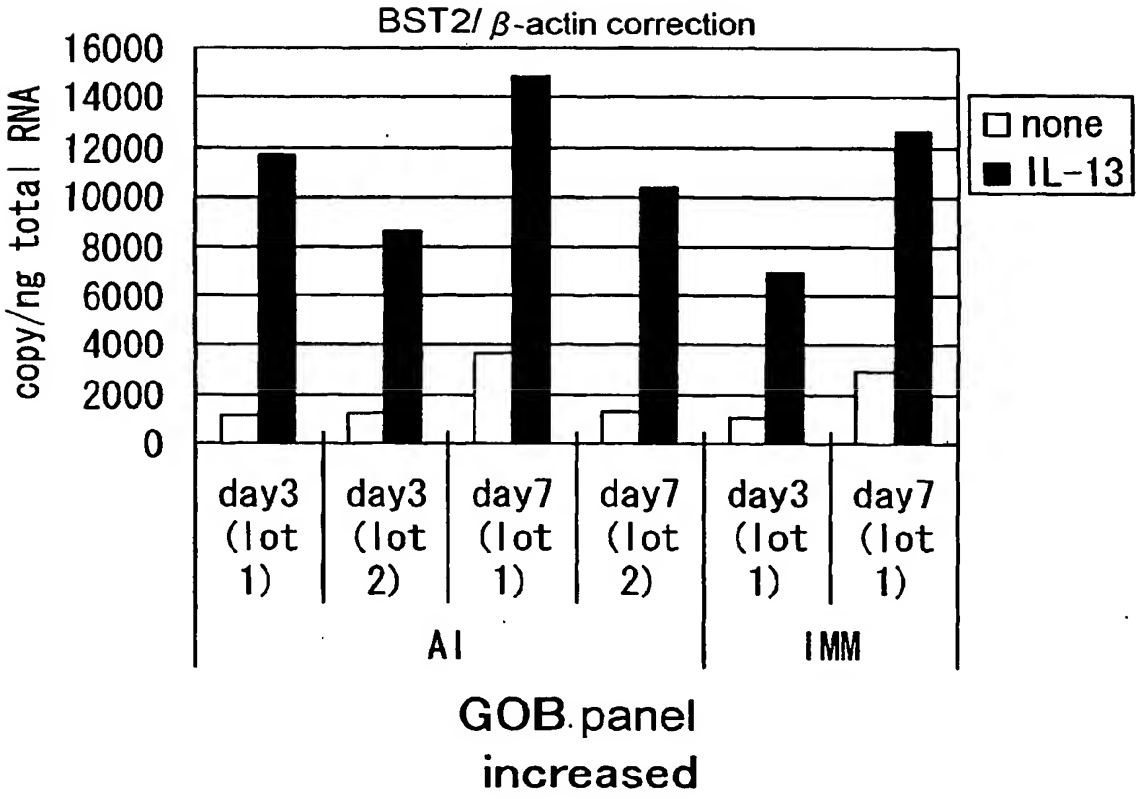
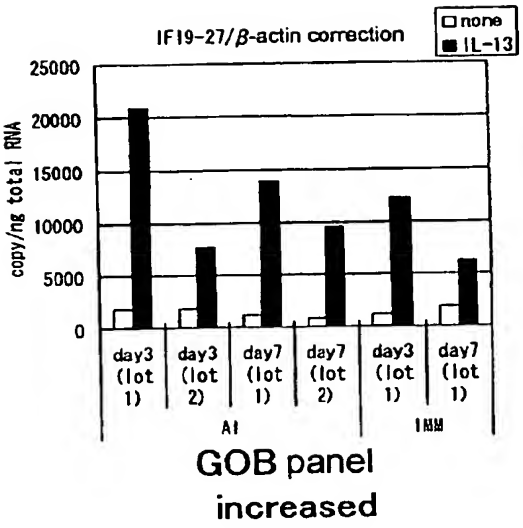
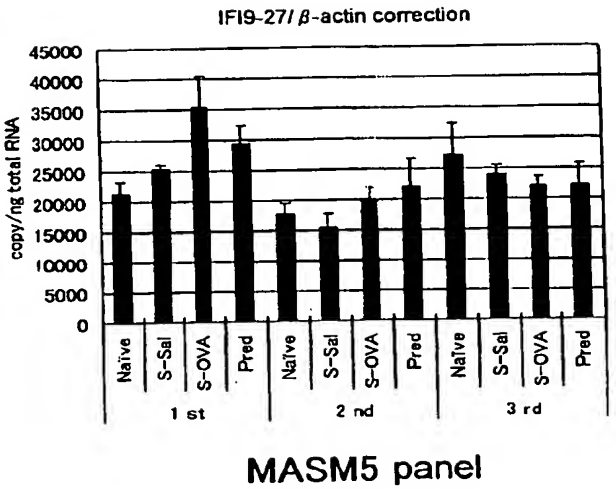


Fig. 58

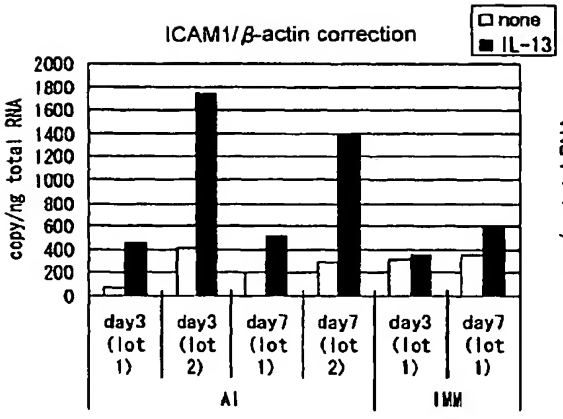


GOB panel
increased

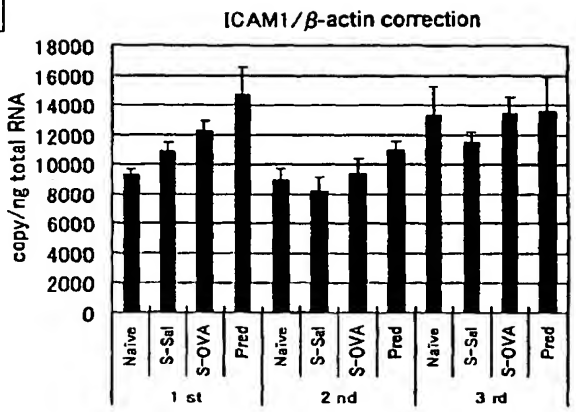


MASM5 panel

Fig. 59

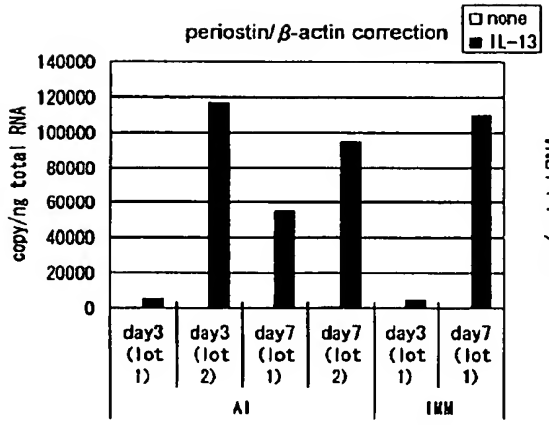


GOB panel increased

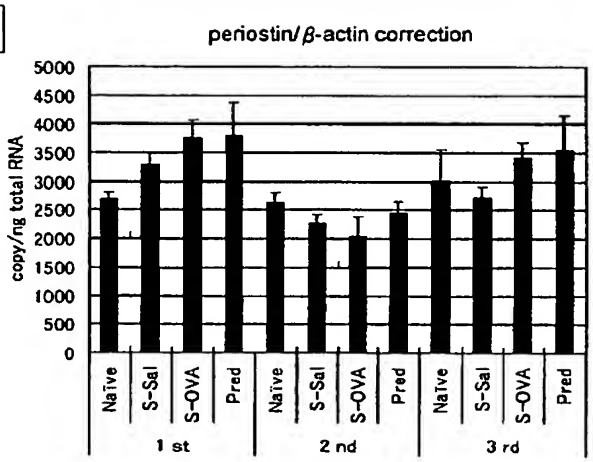


MASM5 panel

Fig. 60

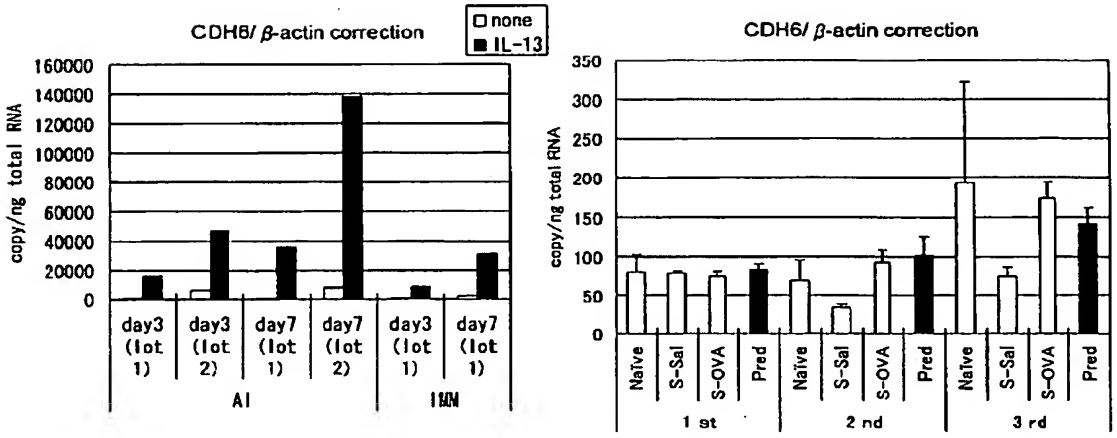


GOB panel
increased



MASM5 panel

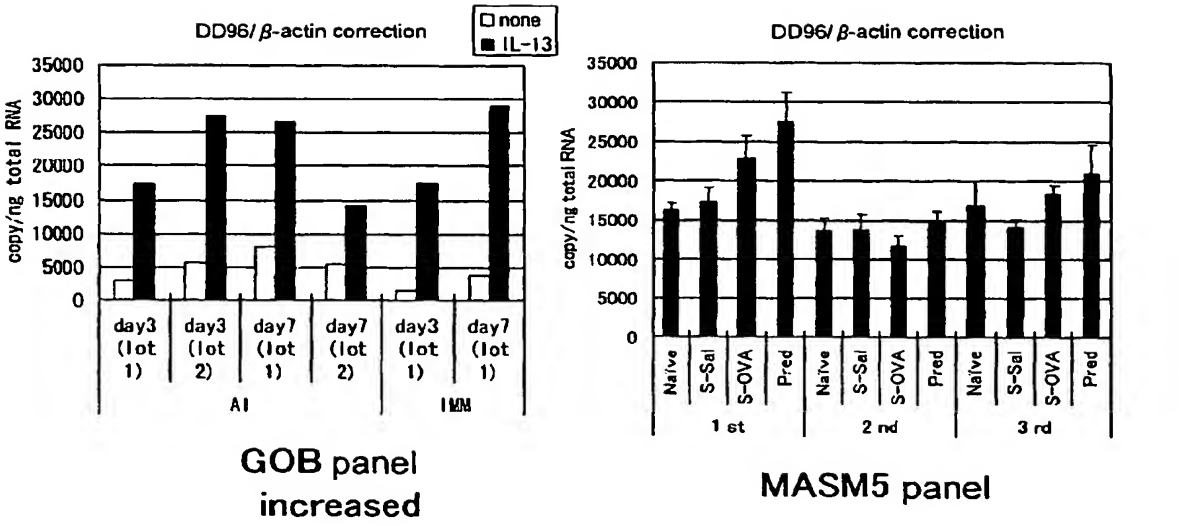
Fig. 61



GOB panel increased

MASM5 panel

Fig. 62



GOB panel increased

MASM5 panel

Fig. 63

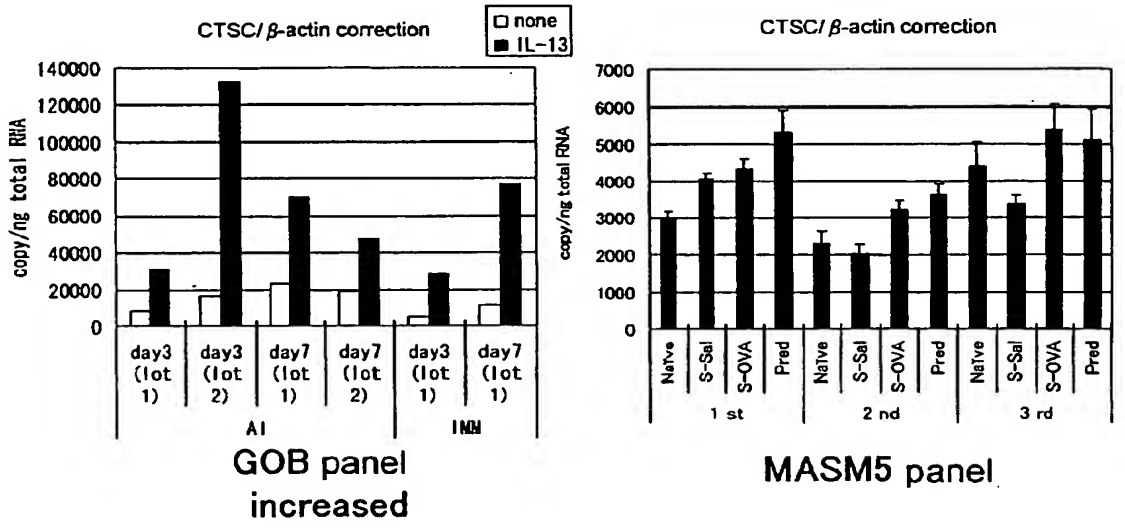
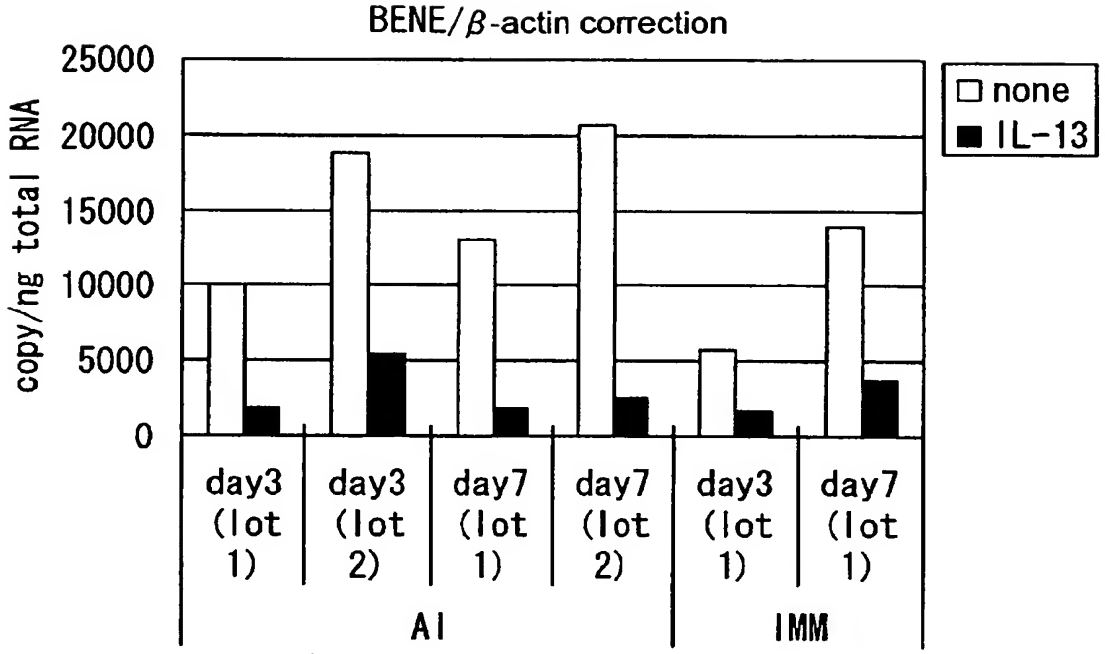


Fig. 64



GOB panel
decreased

Fig. 65

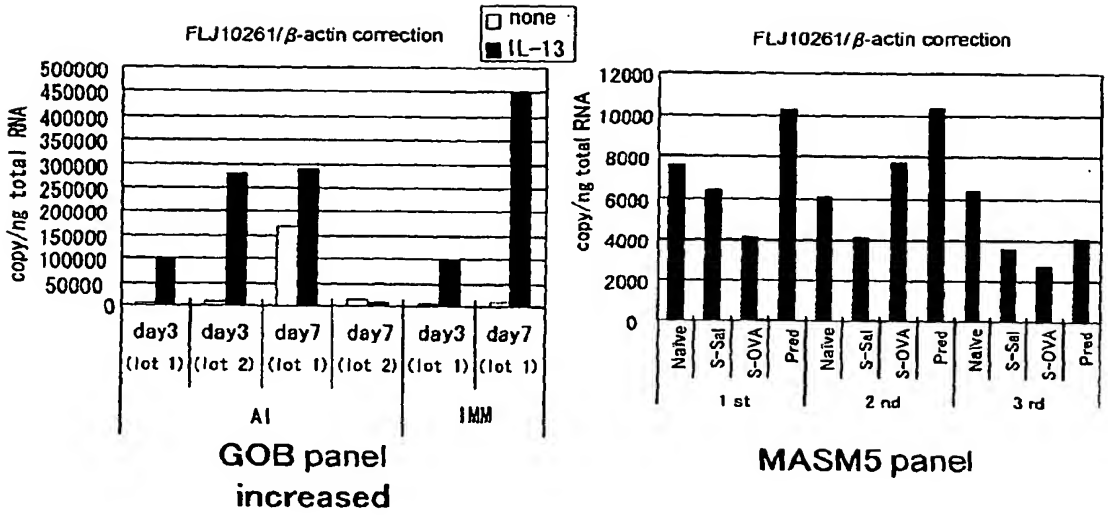
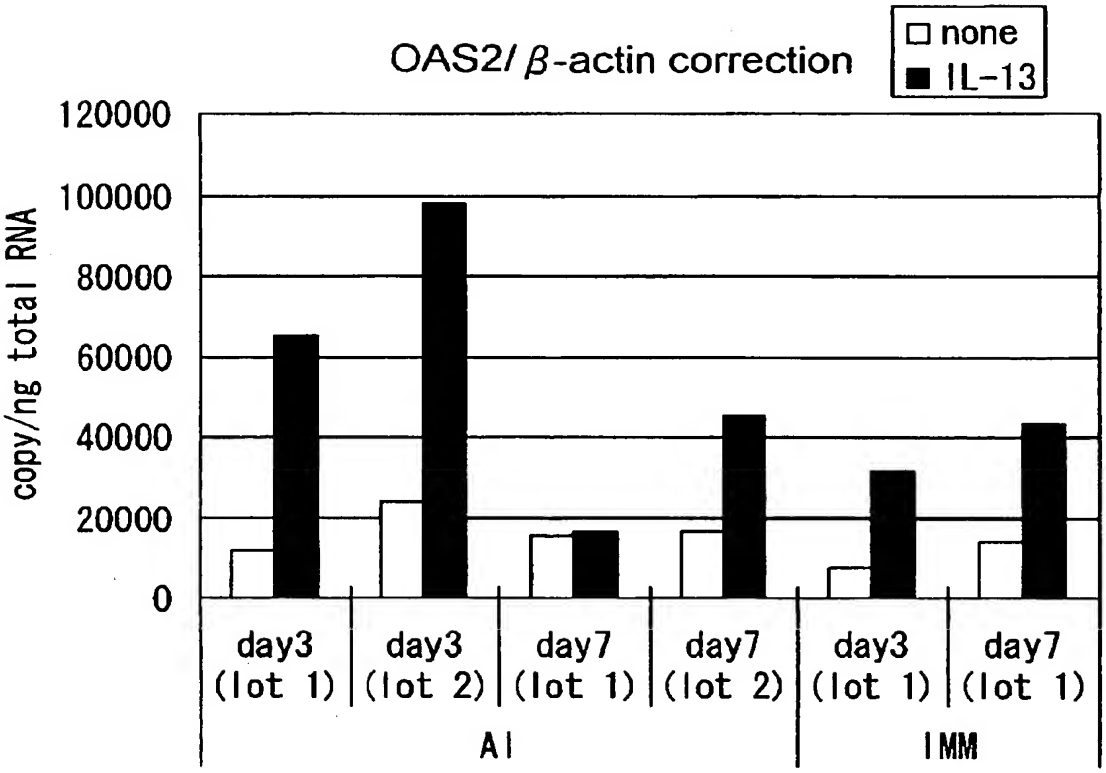
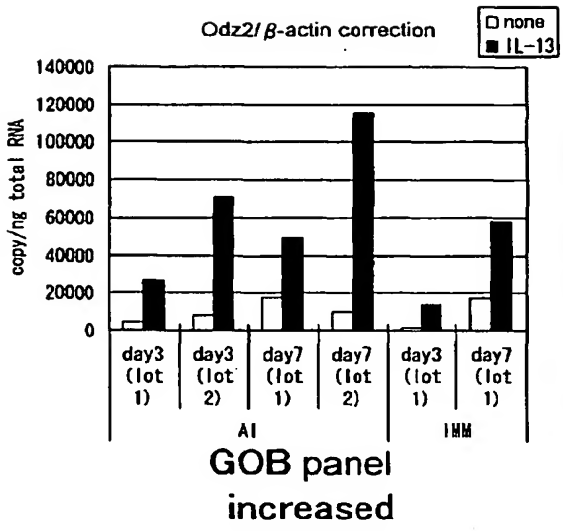


Fig. 66

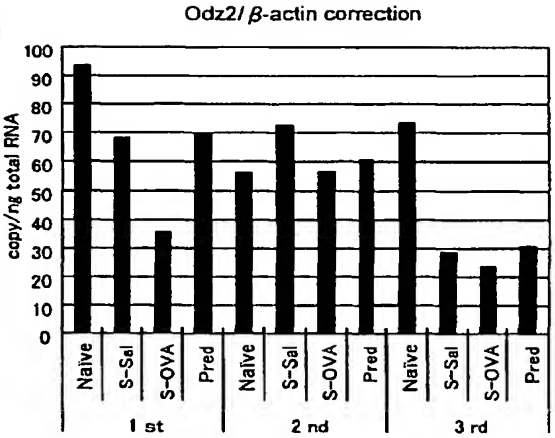


GOB panel increased

Fig. 67

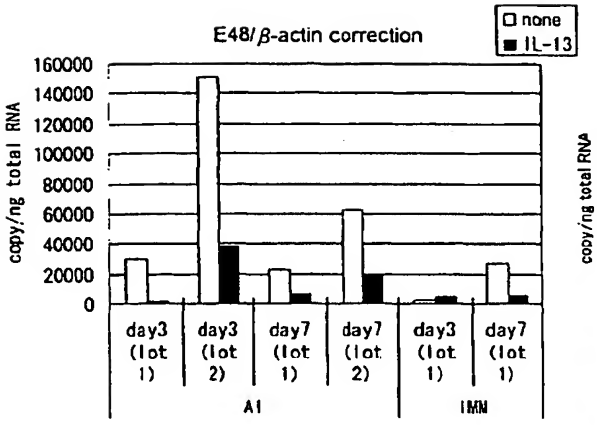


GOB panel increased

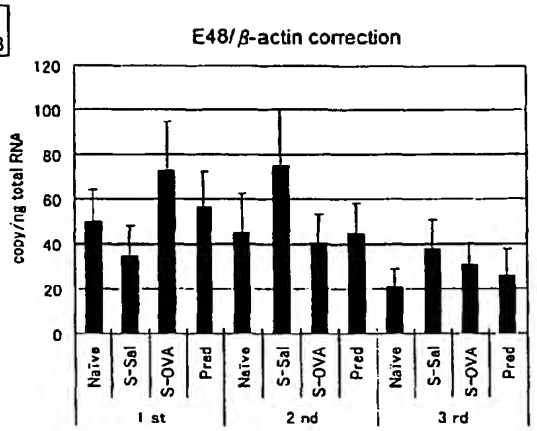


MASM5 panel

Fig. 68

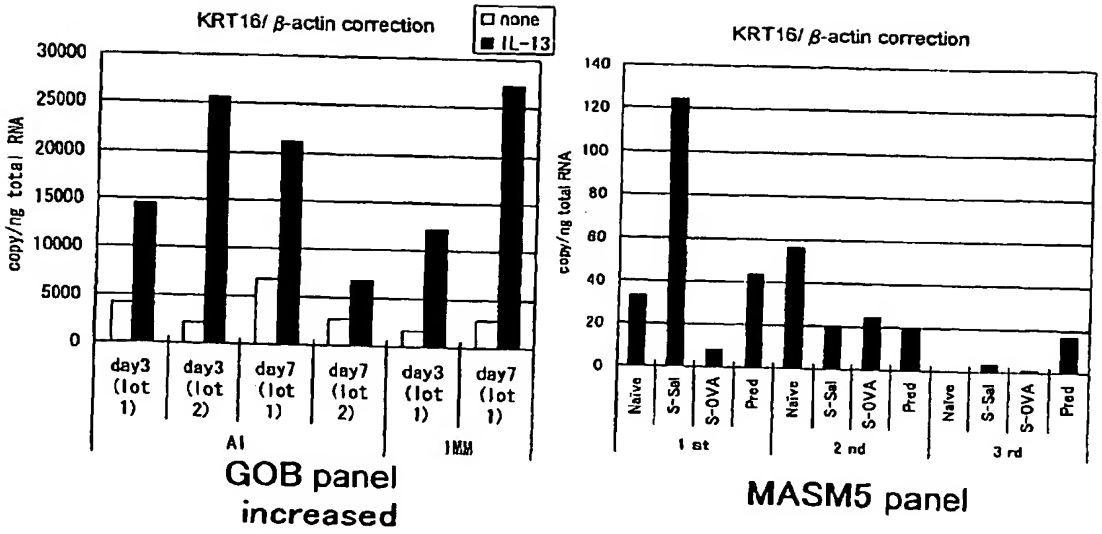


GOB panel
decreased



MASM5 panel

Fig. 69



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(54) Methods of testing for bronchial asthma or chronic obstructive pulmonary disease

(57) An objective of the present invention is to provide a method of testing for bronchial asthma or chronic obstructive pulmonary disease, a method of screening for candidate compounds for treating bronchial asthma or chronic obstructive pulmonary disease, and a pharmaceutical agent for treating bronchial asthma or chronic obstructive pulmonary disease.

The present invention identified genes whose expression levels varied between respiratory epithelial cells that had been stimulated by IL-13 to induce the goblet cell differentiation, and unstimulated respiratory epithelial cells. The respiratory epithelial cells were cultured according to the air interface method. The genes were revealed to be useful as markers for testing for bronchial asthma or chronic obstructive pulmonary disease and screening for therapeutic agents for such diseases. Specifically, the present invention provides methods of testing for bronchial asthma or chronic obstructive pulmonary disease and methods of screening for compounds to treat the diseases based on the comparison of the expression levels of marker genes identified as described above.

EP 1 394 274 A3

European Patent Office

PARTIAL EUROPEAN SEARCH REPORT

which under Rule 45 of the European Patent Convention shall be considered, for the purposes of subsequent proceedings, as the European search report

Application Number EP 03 25 4857

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
Y	WO 02/052006 A (GENOX RES INC ;IZUHARA KENJI (JP); OHTANI NORIKO (JP); SUGITA YUJI) 4 July 2002 (2002-07-04) & EP 1 347 051 A (GENOX RESEARCH, INC.) 4 July 2002 (2002-07-04) * page 3, paragraph 15 - paragraph [0016] * * page 6, paragraph 30 * * page 15, paragraph 111 * * page 16; table 1 * * page 71, line 56 - page 72, line 5 * * page 72, line 6 * * page 72, line 7 * * page 72, lines 11,12 * * page 72, lines 25-29 * * page 72, lines 34-39 * * page 72, lines 42-49 * * page 72, lines 51-56 *	1-4, 7-13, 20-22	C12Q1/68 C12Q1/02 C12N15/11 C12N15/10
X	US 6 090 367 A (KHALIL NASREEN) 18 July 2000 (2000-07-18) * column 16, lines 26-31 *	6	

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TECHNICAL FIELDS SEARCHED (Int.Cl.7)

C12Q
C12N

INCOMPLETE SEARCH

The Search Division considers that the present application, or one or more of its claims, does/do not comply with the EPC to such an extent that a meaningful search into the state of the art cannot be carried out, or can only be carried out partially, for these claims.

Claims searched completely :

Claims searched incompletely :

Claims not searched :

Reason for the limitation of the search:

see sheet C

Place of search	Date of completion of the search	Examiner
Munich	18 December 2003	Helliot, B

CATEGORY OF CITED DOCUMENTS

X : particularly relevant if taken alone
Y : particularly relevant if combined with another document of the same category
A : technological background
O : non-written disclosure
P : intermediate document

T : theory or principle underlying the invention
E : earlier patent document, but published on, or after the filing date
D : document cited in the application
L : document cited for other reasons

& : member of the same patent family, corresponding document

EPO FORM 1503 03.82 (P04C07)

European Patent Office

INCOMPLETE SEARCH
SHEET C

Application Number
EP 03 25 4857

Claim(s) searched incompletely:
23

Reason for the limitation of the search:

Present claim 23 relates to a therapeutic agent for bronchial asthma or COPD, which comprises as an active ingredient a compound being obtainable by any of the screening methods according to claims 7, 20, 21 and 22. However, in the absence of any indication as to the technical feature relating to the nature of the therapeutic agent, a lack of clarity within the meaning of Article 84 EPC arises to such an extend that these sole feature is not sufficient for the skilled person to understand without undue burden the actual scope of the said claims. Consequently, the search has been carried out for those parts of the claims 23 which do refer to the marker gene, the anti-sense corresponding to a portion of the said marker gene, a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect, wherein the marker gene is the thrombospondin-1 gene (SEQ ID N° 25) or an antibody (including fragment or derivative thereof) recognizing a protein encoded by the thrombospondin-1 gene as disclosed in the present description (p. 50, l. 1 - p. 52, l. 10).

European Patent Office

PARTIAL EUROPEAN SEARCH REPORT

Application Number
EP 03 25 4857

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	
X	DIXIT V M ET AL: "CHARACTERIZATION OF A COMPLEMENTARY DNA ENCODING THE HEPARIN AND COLLAGEN BINDING DOMAINS OF HUMAN THROMBOSPONDIN" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES, vol. 83, no. 15, 1986, pages 5449-5453, XP009022127 1986 ISSN: 0027-8424 * page 5451; figure 3 *	5	
Y	HUANG SHIH-WEN ET AL: "Plasma thrombospondin: A novel indicator of platelet activation in allergic asthma" JOURNAL OF ALLERGY AND CLINICAL IMMUNOLOGY, vol. 91, no. 1 PART 2, 1993, page 207, XP009022100 Forty-ninth Annual Meeting of the American Academy of Allergy and Immunology;Chicago, Illinois, USA; March 12-17, 1993 ISSN: 0091-6749 * abstract *	1-4, 7-13, 20-22	TECHNICAL FIELDS SEARCHED (Int.Cl.7)
X	WO 02/39122 A (MILLENNIUM PHARM INC) 16 May 2002 (2002-05-16) * page 60, lines 13-25 * * page 67, lines 28-30 * * page 95 - page 97 *	5,6,27	

EPO FORM 1503 03.82 (P04C10)

European Patent Office

Application Number
EP 03 25 4857

CLAIMS INCURRING FEES

The present European patent application comprised at the time of filing more than ten claims.

☐ Only part of the claims have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims and for those claims for which claims fees have been paid, namely claim(s):

☐ No claims fees have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims.

LACK OF UNITY OF INVENTION

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

see sheet B

☐ All further search fees have been paid within the fixed time limit. The present European search report has been drawn up for all claims.

☐ As all searchable claims could be searched without effort justifying an additional fee, the Search Division did not invite payment of any additional fee.

☐ Only part of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the inventions in respect of which search fees have been paid, namely claims:

☒ None of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims, namely claims:

Claims 1-15, 20-25, 27 (all partially)

European Patent Office

LACK OF UNITY OF INVENTION SHEET B

Application Number
EP 03 25 4857

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

Invention 1: Claims 1-15, 20-25, 27 (all partially)

A method of testing for bronchial asthma or COPD, as defined in claim 1-4, wherein the marker gene comprises the nucleotide sequence of SEQ ID N° 25.

A reagent for testing for bronchial asthma or COPD, as defined in claims 5 or 6; wherein the marker gene comprises the nucleotide sequence of SEQ ID N° 25.

A method of screening for a therapeutic agent for bronchial asthma or COPD, as defined in claims 7-9, wherein the marker gene comprises the nucleotide sequence of SEQ ID N° 25.

A kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or COPD, as defined in claims 10-13, wherein the marker gene comprises the nucleotide sequence of SEQ ID N° 25.

An animal model for bronchial asthma or COPD, as defined in claims 14 and 15, wherein the marker gene comprises the nucleotide sequence of SEQ ID N° 25.

A method of screening for a therapeutic agent for bronchial asthma or COPD, as defined in claims 20-22, wherein the marker gene comprises the nucleotide sequence of SEQ ID N° 25.

A therapeutic agent for bronchial asthma or COPD, as defined in claims 23-25, wherein the marker gene comprises the nucleotide sequence of SEQ ID N° 25.

A DNA chip for testing for bronchial asthma or COPD, as defined in claim 27, wherein the marker gene comprises the nucleotide sequence of SEQ ID N° 25.

Inventions 2-310: Claims 1-15, 20-25, 27 (all partially)

DOCID: <EP_____1394274A3_I_>

European Patent Office

LACK OF UNITY OF INVENTION
SHEET B

Application Number
EP 03 25 4857

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

A method of testing for bronchial asthma or COPD, as defined in claim 1-4, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 26 to 310.

A reagent for testing for bronchial asthma or COPD, as defined in claims 5 or 6; wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 26 to 310.

A method of screening for a therapeutic agent for bronchial asthma or COPD, as defined in claims 7-9, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 26 to 310.

A kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or COPD, as defined in claims 10-13, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 26 to 310.

An animal model for bronchial asthma or COPD, as defined in claims 14 and 15, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 26 to 310.

A method of screening for a therapeutic agent for bronchial asthma or COPD, as defined in claims 20-22, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 26 to 310.

A therapeutic agent for bronchial asthma or COPD, as defined in claims 23-25, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 26 to 310.

A DNA chip for testing for bronchial asthma or COPD, as defined in claim 27, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 26 to 310.

Inventions 311-547: Claims 1-13, 16-17, 20-23, 26-27 (all partially)

European Patent Office

LACK OF UNITY OF INVENTION
SHEET B

Application Number
EP 03 25 4857

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

A method of testing for bronchial asthma or COPD, as defined in claim 1-4, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 311 to 547.

A reagent for testing for bronchial asthma or COPD, as defined in claims 5 or 6; wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 311 to 547.

A method of screening for a therapeutic agent for bronchial asthma or COPD, as defined in claims 7-9, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 311 to 547.

A kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or COPD, as defined in claims 10-13, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 311 to 547.

An animal model for bronchial asthma or COPD, as defined in claims 16 and 17, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 311 to 547.

A method of screening for a therapeutic agent for bronchial asthma or COPD, as defined in claims 20-22, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 311 to 547.

A therapeutic agent for bronchial asthma or COPD, as defined in claims 23-25, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 311 to 547.

A DNA chip for testing for bronchial asthma or COPD, as defined in claim 27, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 311 to 547.

Inventions 548-768: Claims 14-15 , 18-20 , 23 (all partially)

European Patent Office

LACK OF UNITY OF INVENTION
SHEET B

Application Number
EP 03 25 4857

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

An animal model for bronchial asthma or COPD, as defined in claims 14 and 15, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 954 to 1174.

A method for producing an animal model for bronchial asthma or COPD, as defined in claims 18 and 19, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 954 to 1174.

A method of screening for a therapeutic agent for bronchial asthma or COPD, as defined in claim 20, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 954 to 1174.

A therapeutic agent for bronchial asthma or COPD, as defined in claim 23, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 954 to 1174.

Inventions 769-908: Claims 16-20 , 23 (all partially)

European Patent Office

LACK OF UNITY OF INVENTION
SHEET B

Application Number
EP 03 25 4857

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

An animal model for bronchial asthma or COPD, as defined in claims 16 and 17, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 1376 to 1515.

A method for producing an animal model for bronchial asthma or COPD, as defined in claims 18 and 19, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 1376 to 1515.

A method of screening for a therapeutic agent for bronchial asthma or COPD, as defined in claim 20, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 1376 to 1515.

A therapeutic agent for bronchial asthma or COPD, as defined in claim 23, wherein the marker gene comprises any one of the nucleotide sequences of SEQ ID N° 1376 to 1515.

DOCID: <EP_____1394274A3_I_>

ANNEX TO THE EUROPEAN SEARCH REPORT ON EUROPEAN PATENT APPLICATION NO. EP 03 25 4857

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report. The members are as contained in the European Patent Office EDP file on
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

18-12-2003

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 02052006 A	04-07-2002	EP 1347051 A1	24-09-2003
		WO 02052006 A1	04-07-2002
		US 2003152956 A1	14-08-2003
EP 1347051 A	24-09-2003	EP 1347051 A1	24-09-2003
		WO 02052006 A1	04-07-2002
		US 2003152956 A1	14-08-2003
US 6090367 A	18-07-2000	AU 5681996 A	29-11-1996
		EP 0827407 A1	11-03-1998
		CA 2221232 A1	21-11-1996
		WO 9636349 A1	21-11-1996
WO 0239122 A	16-05-2002	AU 2026602 A	21-05-2002
		US 2003166017 A1	04-09-2003
		WO 0239122 A2	16-05-2002

EPO FORM P0459

For more details about this annex : see Official Journal of the European Patent Office, No. 12/82